SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Hadlaczky, Gyula
                  Szalay, Aladar

    (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
    AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES

    (iii) NUMBER OF SEQUENCES: 34

    (iv) CORRESPONDENCE ADDRESS:
      (A) ADDRESSEE: Heller Ehrman White & McAuliffe
      (B) STREET: 4350 La Jolla Village Drive, 6th Floor
      (C) CITY: San Diego
      (D) STATE: CA
      (E) COUNTRY: USA
      (F) ZIP: 92122

    (v) COMPUTER READABLE FORM:
      (A) MEDIUM TYPE: Diskette
      (B) COMPUTER: IBM Compatible
      (C) OPERATING SYSTEM: DOS
      (D) SOFTWARE: FastSEQ Version 1.5

    (vi) CURRENT APPLICATION DATA:
      (A) APPLICATION NUMBER: US/09/836,911
      (B) FILING DATE: 17-APR-2001
      (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
      (A) APPLICATION NUMBER: 08/835,682
      (B) FILING DATE: 10-APR-1997
      (A) APPLICATION NUMBER: 08/695,191
      (B) FILING DATE: 07-AUG-1996
      (A) APPLICATION NUMBER: 08/682,080
      (B) FILING DATE: 15-JUL-1996
      (A) APPLICATION NUMBER: 08/629,822
      (B) FILING DATE: 10-APR-1996

    (viii) ATTORNEY/AGENT INFORMATION:
      (A) NAME: Seidman, Stephanie L
      (B) REGISTRATION NUMBER: 33,779
      (C) REFERENCE/DOCKET NUMBER: 24601-402I

    (ix) TELECOMMUNICATION INFORMATION:
      (A) TELEPHONE: 858-450-8403
      (B) TELEFAX: 858-587-5360
      (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1293 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT    60
TCTCGCCATA TTCCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT   120
TTCGTCATTT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTTCTN   180
GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCCTC   240
GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNCC GTGATTTTCA GTTTTCTCGC   300
CAGATTCCAG GTCCTATAAT GTGCATTTCT CATTTNNCAC GTTTTTCAGT GATTTCGTCA   360
TTTTTTCAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT   420
ATTCCATGTC CTACAATGAT CATTTTTAAT TTTCCACCTT TTCATTTTTC CACGCCATAT   480
TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTTCT CGCCATATTC   540
CAGGTCCTAC AGTGTGCATT CCTCATTTTT CACCTTTTTC ACTGATTTCG TCATTTTTCA   600
AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG   660
TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTTCAAT TTTTCTCGAC ATATTTGACG   720
TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC   780
CTAATAGTGT GCATTCTCA TTTTTCACGT TTTTCAGTGA TTTCGTCATT TTTTCCAGTT   840
GTCAAGGGGA TGTTTCTCAT TTTCCATGAG TGTCAGTTTT CTTGCTATAT TCCATGTCCT   900
ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTTC TCACCATATT TCACGTCCTA   960
AAGTATATAT TTCTCATTTT CCCTGATTTT CAGTTTCCTT GCCATATTCC AGGTCCTACA  1020
GTGTGCATTT CTCATTTTTC ACGTTTTTCA GTAATTTCTT CATTTTTTAA GCCCTCAAAT  1080
GGATGTTTCT CATTTTCCAT GATTTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG  1140
ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTCATCGGC ACATTTCACG TCCTAAAGTG  1200
TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG  1260
CATTTCTCAT TTTTCACGTT TTTCAGTGAA TTC                                1293
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1044 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:
   (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAACT AGACAGAAGG ATTCTCAGAA    60
TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTTGAA GCTTTCTTTT GATAGAGCAG   120
TTTTGAAACA CTCTTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTC   180
CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT   240
TGGGATGTTT CAGTTGAAGT CACAGTGTTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA   300
ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA   360
AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT   420
GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTTG AAACACTCTT   480
TTTGTGGAAT CTGCAAGTGG ATATTTGTCT AGCTTTGAGG ATTTCGTTGG GAAACGGGAT   540
TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG   600
TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGATGTATCT   660
GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA   720
AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGTT   780
GAAGCTTTCT TTTGATAGAG CAGTTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT   840
ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG   900
CATTCCCAGA ATCTTGTTTG TGATGTTTGC ATTCAAGTCA CAGAGTTGAA CATTCCCTTT   960
CAGAGAGCAG GTTTGAACAC TCTTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT  1020
CAGGGGGGAT CCTCTAGAAT TCCT                                         1044
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 2492 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
     (iv) ANTI-SENSE: NO
      (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:
     (ix) FEATURE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCCTTACT ACTCAGATGG GGTGGCCGAG     60
TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT    120
GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA    180
GAGGGTCTGA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG    240
AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT    300
TGCTATCCTG GGGTTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT    360
ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAAACC ATGCCAAGAG    420
AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAATCCAA    480
AGGGCCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT    540
TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA    600
TTTCCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGGCA    660
CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG    720
GATCAACGTT GGTTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGGTTAGGG    780
TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTTAGGG GTTAGGGTTA    840
GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTTATACGCT GTGTTCCACT GGCAATGAAA    900
AGAGTTCTTG TTTTTCCTTC AGCAATTTGT CATTTTTAAA AGAGTTTAGC AATTCTAACA    960
GATATAGACC AGCTGTGCTA TCTCATTGTG GTTTTCAATT GTAACCACAT TGTGGTTTCA   1020
ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG   1080
CATTTCTTGN NTTTNGGCTG TTTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT   1140
GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTC TTCAATATGA GGCTTGCTTT   1200
TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC   1260
TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAAATTC ATTACCAAAC CCAAAGGCAG   1320
ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG   1380
GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTTT CGTCTATATC CATATCATTT   1440
CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTTGGG AAAGACACAG GATAGTGGGC   1500
TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA   1560
GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTCACA TATTAGTAGC ATCTCTAGTG   1620
CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGGA AAAGAGGTCC TATGCAGAAA   1680
GAAACTCCCT AGAACCTGTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA   1740
GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA   1800
CCATAAGTAC AGATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA   1860
ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC   1920
GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG   1980
GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT   2040
TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG   2100
GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA   2160
CTGTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT   2220
TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT   2280
TTGAATTTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG   2340
CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCGCAG GTGGCGGCTG   2400
CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG   2460
ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG                                  2492
```

    (2) INFORMATION FOR SEQ ID NO:4:

      (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 28 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: Genomic DNA

```
         (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
           (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:
          (ix) FEATURE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA                                    28

     (2) INFORMATION FOR SEQ ID NO:5:

           (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 29 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: DNA
         (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
           (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:
          (ix) FEATURE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA                                   29

     (2) INFORMATION FOR SEQ ID NO:6:

           (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 47 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: Gemonic DNA
         (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
           (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:
          (ix) FEATURE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC               47


     (2) INFORMATION FOR SEQ ID NO:7:

           (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 25 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: single
           (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: Genomic DNA
         (iii) HYPOTHETICAL: NO
          (iv) ANTI-SENSE: NO
           (v) FRAGMENT TYPE:
          (vi) ORIGINAL SOURCE:
          (ix) FEATURE:

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
```

CGATTTAAAT TAATTAAGCC CGGGC   25

(2) INFORMATION FOR SEQ ID NO:8:

    (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 27 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
  (iv) ANTI-SENSE: NO
   (v) FRAGMENT TYPE:
  (vi) ORIGINAL SOURCE:
  (ix) FEATURE:

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA   27

(2) INFORMATION FOR SEQ ID NO:9:

    (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 69 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: Genomic DNA
   (D) OTHER INFORMATION IL-2 signal sequence

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT    48
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
 1               5                  10                  15

GTC ACA AAC AGT GCA CCT ACT                                        69
Val Thr Asn Ser Ala Pro Thr
            20
```

(2) INFORMATION FOR SEQ ID NO:10:

    (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 945 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (vi) ORIGINAL SOURCE:

  (ix) FEATURE:

   (A) NAME/KEY: Coding Sequence
   (B) LOCATION: 1...942
   (D) OTHER INFORMATION: Renilla Reinformis Luciferase

  (x) PUBLICATION INFORMATION:

   (H) Document Number: 5,418,155

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG        48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
 1               5                   10                  15

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT        96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
            20                  25                  30

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT       144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
            35                  40                  45

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA       192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
        50                  55                  60

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT       240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65                  70                  75                  80

CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG       288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
            85                  90                  95

TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT       336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
            100                 105                 110

TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG       384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
            115                 120                 125

GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT       432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
            130                 135                 140

CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT       480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145                 150                 155                 160

GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA       528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
            165                 170                 175

ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA       576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
            180                 185                 190

ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA       624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
            195                 200                 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT       672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
            210                 215                 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT       720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225                 230                 235                 240

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG       768
Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
                245                 250                 255

TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC       816
Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
            260                 265                 270
```

-186-

```
GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT        864
Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
        275                     280                 285

TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG        912
Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
        290                     295                 300

TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA                            945
Phe Val Glu Arg Val Leu Lys Asn Glu Gln
305                     310
```

    (2) INFORMATION FOR SEQ ID NO:11:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
     (iv) ANTI-SENSE: NO
      (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:
     (ix) FEATURE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG   30

    (2) INFORMATION FOR SEQ ID NO:12:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
     (iv) ANTI-SENSE: NO
      (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:
     (ix) FEATURE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTCAC   30

    (2) INFORMATION FOR SEQ ID NO:13:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1434 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
     (iv) ANTI-SENSE: NO
      (v) FRAGMENT TYPE:
     (vi) ORIGINAL SOURCE:

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA   60

```
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT    120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC    180
AGGTCCAGAC GACTGACACC ATTAACACTT TGTCAGCCTC AGTGACTACA GTCATAGATG    240
AACAGGCCTC AGCTAATGTC AAGATACAGA GAGGTCTCAT GCTGGTTAAT CAACTCATAG    300
ATCTTGTCCA GATACAACTA GATGTATTAT GACAAATAAC TCAGCAGGGA TGTGAACAAA    360
AGTTTCCGGG ATTGTGTGTT ATTTCCATTC AGTATGTTAA ATTTACTAGG ACAGCTAATT    420
TGTCAAAAAG TCTTTTTCAG TATATGTTAC AGAATTGGAT GGCTGAATTT GAACAGATCC    480
TTCGGGAATT GAGACTTCAG GTCAACTCCA CGCGCTTGGA CCTGTCGCTG ACCAAAGGAT    540
TACCCAATTG GATCTCCTCA GCATTTTCTT TCTTTAAAAA ATGGGTGGGA TTAATATTAT    600
TTGGAGATAC ACTTTGCTGT GGATTAGTGT TGCTTCTTTG ATTGGTCTGT AAGCTTAAGG    660
CCCAAACTAG GAGAGACAAG GTGGTTATTG CCCAGGCGCT TGCAGGACTA GAACATGGAG    720
CTTCCCCTGA TATATGGTTA TCTATGCTTA GGCAATAGGT CGCTGGCCAC TCAGCTCTTA    780
TATCCCACGA GGCTAGTCTC ATTGTACGGG ATAGAGTGAG TGTGCTTCAG CAGCCCGAGA    840
GAGTTGCAAG GCTAAGCACT GCAATGGAAA GGCTCTGCGG CATATATGTG CCTATTCTAG    900
GGGGACATGT CATCTTTCAT GAAGGTTCAG TGTCCTAGTT CCCTTCCCCC AGGCAAAACG    960
ACACGGGAGC AGGTCAGGGT TGCTCTGGGT AAAAGCCTGT GAGCCTGGGA GCTAATCCTG   1020
TACATGGCTC CTTTACCTAC ACACTGGGGA TTTGACCTC ATCTCCACTC TCATTAATAT   1080
GGGTGGCCTA TTTGCTCTTA TTAAAAGGAA AGGGGGAGAT GTTGGGAGCC GCGCCCACAT   1140
TCGCCGTTAC AAGATGGCGC TGACAGCTGT GTTCTAAGTG GTAAACAAAT AATCTGCGCA   1200
TGTGCCGAGG GTGGTTCTTC ACTCCATGTG CTCTGCCTTC CCCGTGACGT CAACTCGGCC   1260
GATGGGCTGC AGCCAATCAG GGAGTGACAC GTCCTAGGCG AAGGAGAATT CTCCTTAATA   1320
GGGACGGGGT TTCGTTCTCT CTCTCTCTCT TGCTTCTCTC TCTTGCTTTT TCGCTCTCTT   1380
GCTTCCCGTA AAGTGATAAT GATTATCATC TACATATCAC AACGTGCGTG GAGG         1434
```

    (2) INFORMATION FOR SEQ ID NO:14:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1400 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: Genomic DNA
      (iii) HYPOTHETICAL: NO
       (iv) ANTI-SENSE: NO
        (v) FRAGMENT TYPE:
       (vi) ORIGINAL SOURCE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```
CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC AGAGCAGCGT TGGGGGATAA     60
TGTCGACATT TCCACTCCCA ATGACGGTGA TGTATAATGC TCAAGTATTC TCCTGCTTTT    120
TTACCACTAA CTAGGAACTG GGTTTGGCCT TAATTCAGAC AGCCTTGGCT CTGTCTGGAC    180
AGGTCCAGAT ACAACTAGAT GTATTATGAC AAATAACTCA GCAGGGATGT GAACAAAAGT    240
TTCGGGATT GCGTGTTATT TCCATCCAGT ATGTTAAATT TACTAGGGCA GCTAATTTGT    300
CAAAAAGTCT TTTCCAGTAT ATGTTACAG ATTGGATGGC TGAATTTGAA CAGATCCTTC    360
GGGAATTGAG ACTTCAGGTC AACTCCACGC GCTTGGACCT GTCCCTGACC AAAGGATTAC    420
CCAATTGGAT CTCCTCAGCA TTTTCTTTCT TTAAAAAATG GGTGGGATTA ATATTATTTG    480
GAGATACACT TTGCTGTGGA TTAGTGTTGC TTCTTTGATT GGTCTGTAAG CTTAAGGCCC    540
AAACTAGGAG AGACAAGGTG GTTATTGCCC AGGCGCTTGC AGGACTAGAA CATGGAGCTT    600
CCCCTGATAT ATCTATGCTT AGGCAATAGG TCGCTGGCCA CTCAGCTCTT ATATCCCATG    660
AGGCTAGTCT CATTGCACGG GATAGAGTGA GTGTGCTTCA GCAGCCCGAG AGAGTTGCAC    720
GGCTAAGCAC TGCAATGGAA AGGCTCTGCG GCATATATGA GCCTATTCTA GGGAGACATG    780
TCATCTTTCA AGAAGGTTGA GTGTCCAAGT GTCCTTCCTC CAGGCAAAAC GACACGGGAG    840
CAGGTCAGGG TTGCTCTGGG TAAAAGCCTG TGAGCCTAAG AGCTAATCCT GTACATGGCT    900
CCTTTACCTA CACACTGGGG ATTTGACCTC TATCTCCACT CTCATTAATA TGGGTGGCCT    960
ATTTGCTCTT ATTAAAAGGA AAGGGGGAGA TGTTGGGAGC CGCGCCCACA TTCGCCGTTA   1020
CAAGATGGCG CTGACAGCTG TGTTCTAAGT GGTAAACAAA TAATCTGCGC ATGCGCCGAG   1080
GGTGGTTCTT CACTCCATGT GCTCTGCCTT CCCCGTGACG TCAACTCGGC CGATGGGCTG   1140
CAGTCAATCA GGGAGTGACA CGTCCTAGGC GAAGGAAAAT TCTCCTTAAT AGGGACGGGG   1200
TTTCGTTTTC TCTCTCTCTT GCTTCGCTCT CTCTTGCTTC TTGCTCTCTT TTCCTGAAGA   1260
TGTAAGAATA AAGCTTTGCC GCAGAAGATT CTGGTCTGTG GTGTTCTTCC TGGCCGGTCG   1320
TGAGAACGCG TCTAATAACA ATTGGTGCCG AAACCCGGGT GATAATGATT ATCATCTACA   1380
TATCACAACG TGCGTGGAGG                                               1400
```

    (2) INFORMATION FOR SEQ ID NO:15:

-188-

```
   (i) SEQUENCE CHARACTERISTICS:
   (A)  LENGTH: 1369 base pairs
   (B)  TYPE: nucleic acid
   (C)  STRANDEDNESS: single
   (D)  TOPOLOGY: linear

  (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
  (iv) ANTI-SENSE: NO
   (v) FRAGMENT TYPE:
  (vi) ORIGINAL SOURCE:

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA CGTTGTGATA TGTAGATGAT AATCATTATC ACTTTACGGG TCCTTTCACT        60
ACAACTGCCA CGAGGCCCCG TGCTCTGGTA ATAGATCTTT GCTGAAAAGG CACACACATG       120
ACACATTACT CAAGGTGGGC TCATCTGAGC TGCAGATTCA GCTTAATATG AATCTTGCCA       180
ATTGTGTGAA ATCATAAATC TTCAAAGTGA CACTCATTGC CAGACACAGG TGCCCACCTT       240
TGGCATAATA AACAAACACA AATTATCTAT TATATAAAGG GTGTTAGAAG ATGCTTTAGA       300
ATACAAATAA ATCATGGTAG ATAACAGTAA GTTGAGAGCT TAAATTTAAT AAAGTGATAT       360
ACCTAATAAA AATTAAATTA AGAAGGTGTG AATATACTAC AGTAGGTAAA TTATTTCATT       420
AATTTATTTT CTTTCTTAAT CCTTTATAAT GTTTCTGCT ATTGTCAATT GCACATCCAT        480
ATGTTCAATT CTTCACTGTA ATGAAGAAAT GTAGTAAATA TACTTTCCGA ACAAGTTGTA       540
TCAAATATGT TACACTTGAT TCCGTGTGTT ACTTATCATT TTATTATTAT ATTGATTGCA       600
TTCCTTCGTT ACTTGATATT ATTACAAGGT ACATATTTAT TCTCTCAGAT CTTCATTATA       660
CTCTAACCAT TTTATAACAT ACTTTATTTA TTCATTTCTT ATGTGTGCTG TGAGGCACAA       720
ATGCCAGAGA GAACTTGAGC AGATAAGAGG ACAAATTGCA AGAGTCAGTT ACCTCCTGCT       780
GTTCCTTGGA AACTCAGGAT CAAATTCAGG TTGTCAGGCT TGGCAGCATG CACTTTTTAC       840
CAGTGCCTCC ATCTTGCTAG CCCTGAACAT CAAGCTTTGC AGACAGACAG GCTACACTAA       900
GTGAACTGGT CATTCACAGC ATGCATGGTG ATTTATTGTT ACTTTCTATT CCATGCCTTT       960
ACTATTTCTA CTAGGTGCTA GCTAGTACTG TATTTCGAGA TAGAAGTTAC TGAAAGAAAA      1020
TTACATTGTT TTCTATAGAT CCTTGATACT CTTTCAGCAG ATATAGAGTT TTAATCAGGT      1080
CCTAGACCCT TTCTTCACTC TTATTAAATA CTAAGTACAA ATTAAGTTTA TCCAAAACAG      1140
TACGGATGTT GATTTTGTGC AGTTCTACTA TGATAATAGT CTAGCTTCAT AAATCTGACA      1200
CACTTATTGG GAATGTTTTT GTTAATAAAA GATTCAGGTG TTACTCTAGG TCAAGAGAAT      1260
ATTAAACATC AGTCCCAAAT TACAAACTTC AATAAAAGAT TTGACTCTCC AGTGGTGGCA      1320
ATATAAAGTG ATAATGATTA TCATCTACAT ATCACAACGT GCGTGGAGG                  1369

  (2)  INFORMATION FOR SEQ ID NO:16:

       (i) SEQUENCE CHARACTERISTICS:
       (A)  LENGTH: 22118 base pairs
       (B)  TYPE: nucleic acid
       (C)  STRANDEDNESS: single
       (D)  TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
     (iii) HYPOTHETICAL: NO
      (iv) ANTI-SENSE: NO
       (v) FRAGMENT TYPE:
      (vi) ORIGINAL SOURCE:

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCCT ATCCCTAATC CAGATTGGTG GAATAACTTG GTATAGATGT TTGTGCATTA        60
AAAACCCTGT AGGATCTTCA CTCTAGGTCA CTGTTCAGCA CTGGAACCTG AATTGTGGCC       120
CTGAGTGATA GGTCCTGGGA CATATGCAGT TCTGCACAGA CAGACAGACA GACAGACAGA       180
CAGACAGACA GACAGACGTT ACAAACAAAC ACGTTGAGCC GTGTGCCAAC ACACACACAA       240
ACACCACTCT GGCCATAATT ATTGAGGACG TTGATTTATT ATTCTGTGTT TGTGAGTCTG       300
TCTGTCTGTC TGTCTGTCTG TCTGTCTGTC TATCAAACCA AAAGAAACCA AACAATTATG       360
CCTGCCTGCC TGCCTGCCTG CCTACACAGA GAAATGATTT CTTCAATCAA TCTAAAACGA       420
CCTCCTAAGT TTGCCTTTTT TCTCTTTCTT TATCTTTTTC TTTTTTCTTT TCTTCTTCCT       480
TCCTTCCTTC CTTCCTTCCT TCCTTCCTTT CTTTCTTTCT TTCTTTCTTT CTTACTTTCT       540
TTCTTTCCTT CTTACATTTA TTCTTTTCAT ACATAGTTTC TTAGTGTAAG CATCCCTGAC       600
TGTCTTGAAG ACACTTTGTA GGCCTCAATC CTTCCTCTGC TTTTCAAATG               660
CTGGCATGAA TGTTGTACCT CACTATGACC AGCTTAGTCT TCAAGTCTGA GTTACTGGAA       720
AGGAGTTCCA AGAAGACTGG TTATATTTTT CATTTATTAT TGCATTTTAA TTAAAATTTA       780
```

                                 -189-

```
ATTTCACCAA  AAGAATTTAG  ACTGACCAAT  TCAGAGTCTG  CCGTTTAAAA  GCATAAGGAA      840
AAAGTAGGAG  AAAAACGTGA  GGCTGTCTGT  GGATGGTCGA  GGCTGCTTTA  GGGAGCCTCG      900
TCACCATTCT  GCACTTGCAA  ACCGGGCCAC  TAGAACCCGG  TGAAGGGAGA  AACCAAAGCG      960
ACCTGGAAAC  AATAGGTCAC  ATGAAGGCCA  GCCACCTCCA  TCTTGTTGTG  CGGGAGTTCA     1020
GTTAGCAGAC  AAGATGGCTG  CCATGCACAT  GTTGTCTTTC  AGCTTGGTGA  GGTCAAAGTA     1080
CAACCGAGTC  ACAGAACAAG  GAAGTATACA  CAGTGAGTTC  CAGGTCAGCG  AGAGTTTACA     1140
CAGAGAAACC  ACATCTTGAA  AAAAACAAAA  AAATAAATTA  AATAAATATA  ATTTAAAAAT     1200
TTAAAAATAG  CCGGGAGTGA  TGGCGCATGT  CTTTAATCCC  AGCTCTCTTC  AGGCAGAGAT     1260
GGGAGGATTT  CTGAGTTTGA  GGCCAGCCTG  GTCTGCAAAG  TGAGTTCCAG  GACAGTCAGG     1320
GCTATACAGA  GAAACCCTGT  CTTGAAAACT  AAACTAAATT  AAACTAAACT  AAACTAAAAA     1380
AATATAAAAT  AAAAATTTTA  AAGAATTTTA  AAAAACTACA  GAAATCAAAC  ATAAGCCCAC     1440
GAGATGGCAA  GTAACTGCAA  TCATAGCAGA  AATATTATAC  ACACACACAC  ACACAGACTC     1500
TGTCATAAAA  TCCAATGTGC  CTTCATGATG  ATCAAATTTC  GATAGTCAGT  AATACTAGAA     1560
GAATCATATG  TCTGAAAATA  AAAGCCAGAA  CCTTTTCTGC  TTTTGTTTTC  TTTTGCCCCA     1620
AGATAGGGTT  TCTCTCAGTG  TATCCCTGGC  ATCCCTGCCT  GGAACTTCCT  TTGTAGGTTT     1680
GGTAGCCTCA  AACTCAGAGA  GGTCCTCTCT  GCCTGCCTGC  CTGCCTGCCT  GCCTGCCTGC     1740
CTGCCTGCCT  GCCTGCCTCA  CTTCTTCTGC  CACCCACACA  ACCGAGTCGA  ACCTAGGATC     1800
TTTATTTCTT  TCTCTTTCTC  TCTTCTTTCT  TTCTTTCTTT  CTTTCTTTCT  TTCTTTCTTT     1860
CTTTCTTTCT  TTCTTATTCA  ATTAGTTTTC  AATGTAAGTG  TGTGTTTGTG  CTCTATCTGC     1920
TGCCTATAGG  CCTGCTTGCC  AGGAGAGGGC  AACAGAACCT  AGGAGAAACC  ACCATGCAGC     1980
TCCTGAGAAT  AAGTGAAAAA  ACAACAAAAA  AAGGAAATTC  TAATCACATA  GAATGTAGAT     2040
ATATGCCGAG  GCTGTCAGAG  TGCTTTTTAA  GGCTTAGTGT  AAGTAATGAA  AATTGTTGTG     2100
TGTCTTTTAT  CCAAACACAG  AAGAGAGGTG  GCTCGGCCTG  CATGTCTGTT  GTCTGCATGT     2160
AGACCAGGCT  GGCCTTGAAC  ACATTAATCT  GTCTGCCTCT  GCTTCCCTAA  TGCTGCGATT     2220
AAAGGCATGT  GCCACCACTG  CCCGGACTGA  TTTCTTCTTT  TTTTTTTTTT  TGGAAAATAC     2280
CTTTCTTTCT  TTTTCTCTCT  CTCTTTCTTC  CTTCCTTCCT  TTCTTTCTAT  TCTTTTTTTC     2340
TTTCTTTTTT  CTTTTTTTTT  TTTTTTTTAA  AATTTGCCTA  AGGTTAAAGG  TGTGCTCCAC     2400
AATTGCCTCA  GCTCTGCTCT  AATTCTCTTT  AAAAAAAAAC  AAACAAAAAA  AAAACCAAAA     2460
CAGTATGTAT  GTATGTATAT  TTAGAAGAAA  TACTAATCCA  TTAATAACTC  TTTTTTCCTA     2520
AAATTCATGT  CATTCTTGTT  CCACAAAGTG  AGTTCCAGGA  CTTACCAGAG  AAACCCTGTG     2580
TTCAAATTTC  TGTGTTCAAG  GTCACCCTGG  CTTACAAAGT  GAGTTCCAAG  TCCGATAGGG     2640
CTACACAGAA  AAACCATATC  TCAGAAAAAA  AAAAGTTCC  AAACACACAC  ACACACAC      2700
ACACACACAC  ACACACACAC  ACACACACAC  ACACACACAG  CGCGCCGCGG  CGATGAGGGG     2760
AAGTCGTGCC  TAAAATAAAT  ATTTTTCTGG  CCAAAGTGAA  AGCAAATCAC  TATGAAGAGG     2820
TACTCCTAGA  AAAAATAAAT  ACAAACGGGC  TTTTTAATCA  TTCCAGCACT  GTTTTAATTT     2880
AACTCTGAAT  TTAGTCTTGG  AAAAGGGGGC  GGGTGTGGGT  GAGTGAGGGC  GAGCGAGCAG     2940
ACGGGCGGGC  GGGCGGGTGA  GTGGCCGGCG  GCGGTGGCAG  CGAGCACCAG  AAAACAACAA     3000
ACCCCAAGCG  GTAGAGTGTT  TTAAAAATGA  GACCTAAATG  TGGTGGAACG  GAGGTCGCCG     3060
CCACCCTCCT  CTTCCACTGC  TTAGATGCTC  CCTTCCCCTT  ACTGTGCTCC  CTTCCCCTAA     3120
CTGTGCCTAA  CTGTGCCTGT  TCCCTCACCC  CGCTGATTCG  CCAGCGACGT  ACTTTGACTT     3180
CAAGAACGAT  TTTGCCTGTT  TTCACCGCTC  CCTGTCATAC  TTTCGTTTTT  GGGTGCCCGA     3240
GTCTAGCCCG  TTCGCTATGT  TCGGGCGGGA  CGATGGGGAC  CGTTTGTGCC  ACTCGGGAGA     3300
AGTGGTGGGT  GGGTACGCTG  CTCCGTCGTG  CGTGCGTGAG  TGCCGGAACC  TGAGCTCGGG     3360
AGACCCTCCG  GAGAGACAGA  ATGATGGAGT  GAATGTGGCG  GCGCGTGACG  GATCTGTATT     3420
GGTTTGTATG  GTTGATCGAG  ACCATTGTCG  GGCGACACCT  AGTGGTGACA  AGTTTCGGGA     3480
ACGCTCCAGG  CCTCTCAGGT  TGGTGACACA  GGAGAGGGAA  GTGCCTGTGG  TGAGGCGACC     3540
AGGGTGACAG  GAGGCCGGGC  AAGCAGGCGG  GAGCGTCTCG  GAGATGGTGT  CGTGTTTAAG     3600
GACGGTCTCT  AACAAGGAGG  TCGTACAGGG  AGATGGCCAA  AGCAGACCGA  GTTGCTGTAC     3660
GCCCTTTTGG  GAAAAATGCT  AGGGTTGGTG  GCAACGTTAC  TAGGTCGACC  AGAAGGCTTA     3720
AGTCCTACCC  CCCCCCCCCT  TTTTTTTTTT  TTTCCTCCAG  AAGCCCTCTC  TTGTCCCCGT     3780
CACCGGGGGC  ACCGTACATC  TGAGGCCGAG  AGGACGCGAT  GGGCCCGGCT  TCCAAGCCGG     3840
TGTGGCTCGG  CCAGCTGGCG  CTTCGGGTCT  TTTTTTTTTT  TTTTTTTTTT  TTTTCCTCCA     3900
GAAGCCTTGT  CTGTCGCTGT  CACCGGGGGC  GCTGTACTTC  TGAGGCCGAG  AGGACGCGAT     3960
GGGCCCGGC  TTCCAAGCCG  GTGTGGCTCG  GCCAGCTGGA  GCTTCGGGTC  TTTTTTTTTT     4020
TTTTTTTTTT  TTTTTTTCTC  CAGAAGCCTT  GTCTGTCGCT  GTCACCGGGG  GCGCTGTACT     4080
TCTGAGGCCG  AGAGGACGCG  ATGGGTCGGC  TTCCAAGCCG  ATGTGCGGGG  GCCAGCTGGA     4140
GCTTCGGGTT  TTTTTTTTTC  CTCCAGAAGC  CCTCTCTTGT  CCCCGTCACC  GGGGGCGCTG     4200
TACTTCTGAG  GCCGAGAGGA  CGTGATGGGC  CCGGGTTCCA  GGCGGATGTC  GCCCGGTCAG     4260
CTGGAGCTTT  GGATCTTTTT  TTTTTTTTTT  CCTCCAGAAG  CCCTCTCTTG  TCCCCGTCAC     4320
CGGGGGCACC  TTACATCTGA  GGGCGAGAGG  ACGTGATGGG  TCCGGCTTCC  AAGCCGATGT     4380
GGCGGGGCCA  GCTGGAGCTT  CGGGTTTTTT  TTTTTCCTC  CAGAAGCCCT  CTCTTGTCCC     4440
CGTCACCGGG  GGCGCTGTAC  TTCTGAGGCC  GAGAGGACGT  GATGGGCCCG  GGTTCCAGGC     4500
GGATGTCGCC  CGGTCAGCTG  GAGCTTTGGA  TCATTTTTTT  TTTCCCTCC  AGAAGCCCTC     4560
TCTTGTCCCC  GTCACCGGGG  GCACCGTACA  TCTGAGGCCG  AGAGGACACG  ATGGGCCTGT     4620
CTTCCAAGCC  GATGTGGCCC  GGCCAGCTGG  AGCTTCGGGT  CTTTTTTTTT  TTTTTTCCTC     4680
CAGAAGCCTT  GTCTGTCGCT  GTCACCCGGG  GCGCTGTACT  TCTGAGGCCG  AGAGGACGCG     4740
ATGGGCCCGG  CTTCCAAGCC  GGTGTGGCTC  GGCCAGCTGG  AGCTTCGGGT  CTTTTTTTTT     4800
```

```
TTTTTTTTTT TTCCTCCAGA AACCTTGTCT GTCGCTGTCA CCCGGGGCGC TTGTACTTCT    4860
GATGCCGAGA GGACGCGATG GGCCCGTCTT CCAGGCCGAT GTGGCCCGGT CAGCTGGAGC    4920
TTTGGATCTT TTTTTTTTTT TTTTCCTCCA GAAGCCCTCT CTTGTCCCCG TCACCGGGGG    4980
CACCTTACAT CTGAGGCCTA GAGGACACGA TGGGCCCGGG TTCCAGGCCG ATGTGGCCCG    5040
GTCAGCTGGA GCTTTGGATC TTTTTTTTTT TTTTCTTCCA GAAGCCCTCT TGTCCCCGTC    5100
ACCGGTGGCA CTGTACATCT GAGGCGGAGA GGACATTATG GGCCCGGCTT CCAATCCGAT    5160
GTGGCCCGGT CAGCTGGAGC TTTGGATCTT ATTTTTTTTT TAATTTTTTC TTCCAGAAGC    5220
CCTCTTGTCC CTGTCACCGG TGGCACGGTA CATCTGAGGC CGAGAGGACA TTATGGGCCC    5280
GGCTTCCAGG CCGATGTGGC CCGGTCAGCT GGAGCTTTGG ATCTTTTTTT TTTTTTTTCT    5340
TTTTCCTCC AGAAGCCCTC TCTGTCCCTG TCACCGGGGG CCCTGTACGT CTGAGGCCGA    5400
GGGAAAGCTA TGGGCGCGGT TTTCTTTCAT TGACCTGTCG GTCTTATCAG TTCTCCGGGT    5460
TGTCAGGGTC GACCAGTTGT TCCTTTGAGG TCCGGTTCTT TTCGTTATGG GGTCATTTTT    5520
GGGCCACCTC CCCAGGTATG ACTTCCAGGC GTCGTTGCTC GCCTGTCACT TTCCTCCCTG    5580
TCTCTTTTAT GCTTGTGATC TTTTCTATCT GTTCCTATTG GACCTGGAGA TAGGTACTGA    5640
CACGCTGTCC TTTCCCTATT AACACTAAAG GACACTATAA AGAGACCCTT TCGATTTAAG    5700
GCTGTTTTGC TTGTCCAGCC TATTCTTTTT ACTGGCTTGG GTCTGTCGCG GTGCCTGAAG    5760
CTGTCCCCGA GCCACGCTTC CTGCTTTCCC GGGCTTGCTG CTTGCGTGTG CTTGCTGTGG    5820
GCAGCTTGTG ACAACTGGGC GCTGTGACTT TGCTGCGTGT CAGACGTTTT TCCCGATTTC    5880
CCCGAGGTGT CGTTGTCACA CCTGTCCCGG TTGGAATGGT GGAGCCAGCT GTGGTTGAGG    5940
GCCACCTTAT TTCGGCTCAC TTTTTTTTTT TTTTTTTCTC TTGGAGTCCC GAACCTCCGC    6000
TCTTTCTCT TCCCGGTCTT TCTTCCACAT GCCTCCCGAG TGCATTTCTT TTTGTTTTTT    6060
TTCTTTTTTT TTTTTTTTTT TTGGGGAGGT GGAGAGTCCC GAGTACTTCA CTCCTGTCTG    6120
TGGTGTCCAA GTGTTCATGC CACGTGCCTC CCGAGTGCAC TTTTTTTTGT GGCAGTCGCT    6180
CGTTGTGTTC TCTTGTTCTG TGTCTGCCCG TATCAGTAAC TGTCTTGCCC CGCGTGTAAG    6240
ACATTCCTAT CTCGCTTGTT TCTCCCGATT GCGCGTCGTT GCTCACTCTT AGATCGATGT    6300
GGTGCTCCGG AGTTCTCTTC GGGCCAGGGC CAAGCCGCGC CAGGCGAGGG ACGGACATTC    6360
ATGGCGAATG GCGGGCCGTC TTCTCGTTCT GCCAGCGGGC CCTCGTCTCT CCACCCCATC    6420
CGTCTGCCGG TGGTGTGTGG AAGGCAGGGG TGCGGCTCTC CGGCCCGACG CTGCCCCGCG    6480
CGCACTTTTC TCAGTGGTTC GCGTGGTCCT TGTGGATGTG TGAGGCGCCC GGTTGTGCCC    6540
TCACGTGTTT CACTTTGGTC GTGTCTCGCT TGACCATGTT CCCAGAGTCG GTGGATGTGG    6600
CCGGTGGCGT TGCATACCCT TCCCGTCTGG TGTGTGCACG CGCTGTTTCT TGTAAGCGTC    6660
GAGGTGCTCC TGGAGCGTTC CAGGTTTGTC TCCTAGGTGC CTGCTTCTGA GCTGGTGGTG    6720
GCGCTCCCCA TTCCCTGGTG TGCCTCCGGT GCTCCGTCTG GCTGTGTGCC TTCCCGTTTG    6780
TGTCTGAGAA GCCCGTGAGA GGGGGGTCGA GGAGAGAAGG AGGGGCAAGA CCCCCCTTCT    6840
TCGTCGGGTG AGGCGCCCAC CCCGCGACTA GTACGCCTGT GCGTAGGGCT GGTGCTGAGC    6900
GGTCGGCGGCT GGGGTTGGAA AGTTTCTCGA GAGACTCATT GCTTTCCCGT GGGGAGCTTT    6960
GAGAGGCCTG GCTTTCGGGG GGGACCGGTT GCAGGGTCTC CCCTGTCCGC GGATGCTCAG    7020
AATGCCCTTG GAAGAGAACC TTCCTGTTGC CGCAGACCCC CCCGCGCGGT CGCCCGCGTG    7080
TTGGTCTTCT GGTTTCCCTG TGTGCTCGTC GCATGCATCC TCTCTCGGTG GCCGGGGCTC    7140
GTCGGGGTTT TGGGTCCGTC CCGCCCTCAG TGAGAAAGTT TCCTTCTCTA GCTATCTTCC    7200
GGAAAGGGTG CGGGCTTCTT ACGGTCTCGA GGGGTCTCTC CCGAATGGTC CCCTGGAGGG    7260
CTCGCCCCCT GACCGCCTCC CGCGCGCGCA GCGTTTGCTC TCTCGTCTAC CGCGGCCCGC    7320
GGCCTCCCCG CTCCGAGTTC GGGGAGGGAT CACGCGGGGC AGAGCCTGTC TGTCGTCCTG    7380
CCGTTGCTGC GGAGCATGTG GCTCGGCTTG TGTGGTTGGT GGCTGGGGAG AGGGCTCCGT    7440
GCACACCCCC GCGTGCGCGT ACTTTCCTCC CCTCCTGAGG GCCGCCGTGC GGACGGGGTG    7500
TGGGTAGGCG ACGGTGGGCT CCCGGGTCCC CACCCGTCTT CCCGTGCCTC ACCCGTGCCT    7560
TCCGTCGCGT GCGTCCCTCT CGCTCGCGTC CACGACTTTG GCCGCTCCCG CGACGGCGGC    7620
CTGCGCCGCG CGTGGTGCGT GCTGTGTGCT TCTCGGGCTG TGTGGTTGTG TCGCCTCGCC    7680
CCCCCCTTCC CGCGGCAGCG TTCCCACGGC TGGCGAAATC GCGGGAGTCC TCCTTCCCCT    7740
CCTCGGGGTC GAGAGGGTCC GTGTCTGGCG TTGATTGATC TCGCTCTCGG GGACGGGACC    7800
GTTCTGTGGG AGAACGGCTG TTGGCCGCGT CCGGCGCGAC GTCGGACGTG GGGACCCACT    7860
GCCGCTCGGG GGTCTTCGTC GGTAGGCATC GGTGTGTCGG CATCGGTCTC TCTCTCGTGT    7920
CGGTGTCGCC TCCTCGGGCT CCCGGGGGGC CGTCGTGTTT CGGGTCGGCT CGGCGCTGCA    7980
GGTGTGGTGG GACTGCTCAG GGGAGTGGTG CAGTGTGATT CCCGCCGGTT TTGCCTCGCG    8040
TGCCCTGACC GGTCCGACGC CCGAGCGCTT CTCCGTGCCC TTGTGAGGAC CCCCTTCCGG    8100
GAGGGGCCCG TTTCGGCCGC CCTTGCCGTC GTCGCCGCC CTCGTTCTGC TGTGTCGTTC    8160
CCCCCTCCCC GCTCGCCGCA GCCGGTCTTT TTTCCTCTCT CCCCCCCTCT CCTCTGACTG    8220
ACCCGTGGCC GTGCTGTCGG ACCCCCCGCA TGGGGCGGC CGGGCACGTA CGCGTCCGGG    8280
CGGTCACCGG GGTCTTGGGG GGGGGCCGAG GGGTAAGAAA GTCGGCTCGG CGGGCGGGAG    8340
GAGCTGTGGT TTGGAGGGCG TCCCGGCCCC GCGGCCGTGG CGGTGTCTTG CGCGGTCTTG    8400
GAGAGGGCTG CGTGCGAGGG GAAAAGGTTG CCCCGCGAGG GCAAAGGGAA AGAGGCTAGC    8460
AGTGGTCATT GTCCCGACGG TGTGGTGGTC TGTTGGCCGA GGTGCGTCTG GGGGGCTCGT    8520
CCGGCCCTGT CGTCCGTCGG GAAGGCGCGT GTTGGGGCCT GCCGGAGTGC CGAGGTGGGT    8580
ACCCTGGCGG TGGGATTAAC CCCGCGCGCG TGTCCCGGTG TGGCGGTGGG GGCTCCGGTC    8640
GATGTCTACC TCCCTCTCCC CGAGGTCTCA GGCCTTCTCC GCGCGGGCTC TCGGCCCTCC    8700
CCTCGTTCCT CCCTCTCGCG GGGTTCAAGT CGCTCGTCGA CCTCCCCTCC TCCGTCCTTC    8760
CATCTCTCGC GCAATGGCGC CGCCCGAGTT CACGGTGGGT TCGTCCTCCG CCTCCGCTTC    8820
```

```
TCGCCGGGGG CTGGCCGCTG TCCGGTCTCT CCTGCCCGAC CCCCGTTGGC GTGGTCTTCT  8880
CTCGCCGGCT TCGCGGACTC CTGGCTTCGC CCGGAGGGTC AGGGGGCTTC CCGGTTCCCC  8940
GACGTTGCGC CTCGCTGCTG TGTGCTTGGG GGGGGCCCGC TGCGGCCTCC GCCCGCCCGT  9000
GAGCCCCTGC CGCACCCGCC GGTGTGCGGT TTCGCGCCGC GGTCAGTTGG GCCCTGGCGT  9060
TGTGTCGCGT CGGGAGCGTG TCCGCCTCGC GGCGGCTAGA CGCGGGTGTC GCCGGGCTCC  9120
GACGGGTGGC CTATCCAGGG CTCGCCCCCG CCGACCCCCG CCTGCCCGTC CCGGTGGTGG  9180
TCGTTGGTGT GGGGAGTGAA TGGTCGCTACC GGTCATTCCC TCCCGCGTGG TTTGACTGTC  9240
TCGCCGGTGT CGCGCTTCTC TTTCCGCCAA CCCCCACGCC AACCCACCAC CCTGCTCTCC  9300
CGGCCCGGTG CGGTCGACGT TCCGGCTCTC CCGATGCCGA GGGGTTCGGG ATTTGTGCCG  9360
GGGACGGAGG GGAGAGCGGG TAAGAGAGGT GTCGGAGAGC TGTCCCGGGG CGACGCTCGG  9420
GTTGGCTTTG CCGCGTGCGT GTGCTCGCGG ACGGGTTTTG TCGGACCCCG ACGGGGTCGG  9480
TCCGGCCGCA TGCACTCTCC CGTTCCGCGC GAGCGCCCGC CCGGCTCACC CCCGGTTTGT  9540
CCTCCCGCGA GGCTCTCCGC CGCCGCCGCC TCCTCCTCCT CTCTCGCGCT CTCTGTCCCG  9600
CCTGGTCCTG TCCCACCCCC GACGCTCCGC TCGCGCTTCC TTACCTGGTT GATCCTGCCA  9660
GGTAGCATAT GCTTGTCTCA AAGATTAAGC CATGCATGTC TAAGTACGCA CGGCCGGTAC  ⌐9720
AGTGAAACTG CGAATGGCTC ATTAAATCAG TTATGGTTCC TTTGGTCGCT CGCTCCTCTC  9780
CTACTTGGAT AACTGTGGTA ATTCTAGAGC TAATACATGC CGACGGGCGC TGACCCCCCT  9840
TCCCGGGGGG GGATGCGTGC ATTTATCAGA TCAAAACCAA CCCGGTGAGC TCCCTCCCGG  9900
CTCCGGCCGG GGGTCGGGCG CCGGCGGCTT GGTGACTCTA GATAACCTCG GGCCGATCGC  9960
ACGCCCCCCG TGGCGGCGAC GACCCATTCG AACGTCTGCC CTATCAACTT TCGATGGTAG  10020
TCGCCGTGCC TACCATGGTG ACCACGGGTG ACGGGGAATC AGGGTTCGAT TCCGGAGAGG  10080
GAGCCTGAGA AACGGCTACC ACATCCAAGG AAGGCAGCAG GCGCGCAAAT TACCCACTCC  10140
CGACCCGGGG AGGTAGTGAC GAAAAATAAC AATACAGGAC TCTTTCGAGG CCCTGTAATT  10200
GGAATGAGTC CACTTTAAAT CCTTTAACGA GGATCCATTG GAGGGCAAGT CTGGTGCCAG  10260
CAGCCGCGGT AATTCCAGCT CCAATAGCGT ATATTAAAGT TGCTGCAGTT AAAAAGCTCG  10320
TAGTTGGATC TTGGGAGCGG GCGGGCGGTC CGCCGCGAGG CGAGTCACCG CCCGTCCCCG  10380
CCCCTTGCCT CTCGGCGCCC CCTCGATGCT CTTAGCTGAG TGTCCCGCGG GGCCCGAAGC  10440
GTTTACTTTG AAAAAATTAG AGTGTTCAAA GCAGGCCCGA GCCGCCTGGA TACCGCAGCT  10500
AGGAATAATG GAATAGGACC GCGGTTCTAT TTTGTTGGTT TTCGGAACTG AGGCCATGAT  10560
TAAGAGGGAC GGCCGGGGGC ATTCGTATTG CGCCGCTAGA GGTGAAATTC TTGGACCGGC  10620
GCAAGACGGA CCAGAGCGAA AGCATTTGCC AAGAATGTTT TCATTAATCA AGAACGAAAG  10680
TCGGAGGTTC GAAGACGATC AGATACCGTC GTAGTTCCGA CCATAAACGA TGCCGACTGG  10740
CGATGCGGCG GCGTTATTCC CATGACCCGC CGGGCAGCTT CCGGGAAACC AAAGTCTTTG  10800
GGTTCCGGGG GGAGTATGGT TGCAAAGCTG AAACTTAAAG GAATTGACGG AAGGGCACCA  10860
CCAGGAGTGG GCCTGCGGCT TAATTTGACT CAACACGGGA AACCTCACCC GGCCCGGACA  10920
CGGACAGGAT TGACAGATTG ATAGCTCTTT CTCGATTCCG TGGGTGGTGG TGCATGGCCG  10980
TTCTTAGTTG GTGGAGCGAT TTGTCTGGTT AATTCCGATA ACGAACGAGA CTCTGGCATG  11040
CTAACTAGTT ACGCGACCCC CGAGCGGTCG GCGTCCCCCA ACTTCTTAGA GGGACAAGTG  11100
GCGTTCAGCC ACCCGAGATT GAGCAATAAC AGGTCTGTGA TGCCCTTAGA TGTCCGGGGC  11160
TGCACGCGCG CTACACTGAC TGGCTCAGCG TGTGCCTACC CTGCGCCGGC AGGCGCGGGT  11220
AACCCGTTGA ACCCCATTCG TGATGGGGAT CGGGGATTGC AATTATTCCC CATGAACGAG  11280
GAATTCCCAG TAAGTGCGGG TCATAAGCTT GCGTTGATTA AGTCCCTGCC CTTTGTACAC  11340
ACCGCCCGTC GCTACTACCG ATTGGATGGT TTAGTGAGGC CCTCGGATCG GCCCCGCCGG  11400
GGTCGGCCCA CGGCCCTGGC GGAGCGCTGA GAAGACGGTC GAACTTGACT ATCTAGAGGA  11460
AGTAAAAGTC GTAACAAGGT TTCCGTAGGT GAACCTGCGG AAGGATCATT AAACGGGAGA  11520
CTGTGGAGGA GCGGCGGCGT GGCCCGCTCT CCCCGTCTTG TGTGTGTCCT CGCCGGGAGG  11580
CGCGTGCGTC CCGGGTCCCG TCGCCCGCGT GTGGAGCGAG GTGTCTGGAG TGAGGTGAGA  11640
GAAGGGGTGG GTGGGGTCGG TCTGGGTCCG TCTGGGACCG CCTCCGATTT CCCCTCCCCC  11700
TCCCCTCTCC CTCGTCCGGC TCTGACCTCG CCACCCTACC GCGGCGGCGG CTGCTCGCGG  11760
GCGTCTTGCC TCTTTCCCGT CCGGCTCTTC CGTGTCTACG AGGGGCGGTA CGTCGTTACG  11820
GGTTTTTGAC CCGTCCCGGG GGCGTTCGGT CGTCGGGGCG CGCGCTTTGC TCTCCCGGCA  11880
CCCATCCCCG CCGCGGCTCT GGCTTTTCTA CGTTGGCTGG GGCGGTTGTC GCGTGTGGGG  11940
GGATGTGAGT GTCGCGTGTG GGCTCGCCCG TCCCGATGCC ACGCTTTTCT GGCCTCGCGT  12000
GTCCTCCCCG CTCCTGTCCC GGGTACCTAG CTGTCGCGTT CCGGCGCGGA GGTTAAGGA  12060
CCCCGGGGGG GTCGCCCTGC CGCCCCCAGG GTCGGGGGGC GGTGGGGCCC GTAGGGAAGT  12120
CGGTCGTTCG GGCGGCTCTC CCTCAGACTC CATGACCCTC CTCCCCCCGC TGCCGCCGTT  12180
CCCGAGGCGG CGGTCGTGTG CGGGGGTGGA TGTCTGGAGC CCCCTCGGGC GCCGTGGGGG  12240
CCCGACCCGC GCCGCCGGCT TGCCCGATTT CCGCGGGTCG GTCCTGTCGG TGCCGGTCGT  12300
GGGTTCCCGT GTCGTTCCCG TGTTTTTCCG CTCCCGACCC TTTTTTTTTC CTCCCCCCCA  12360
CACGTGTCTC GTTTCGTTCC TGCTGGCCGG CCTGAGGCTA CCCCTCGGTC CATCTGTTCT  12420
CCTCTCTCTC CGGGGAGAGG AGGGCGGTGG TCGTTGGGGG ACTGTGCCGT CGTCAGCACC  12480
CGTGAGTTCG CTCACACCCG AAATACCGAT ACGACTCTTA GCGGTGGATC ACTCGGCTCG  12540
TGCGTCGATG AAGAACGCAG CTAGCTGCGA GAATTAATGT GAATTGCAGG ACACATTGAT  12600
CATCGACACT TCGAACGCAC TTGCGGCCCC GGGTTCCTCC CGGGGCTACG CCTGTCTGAG  12660
CGTCGGTTGA CGATCAATCG CGTCACCCGC TGCGGTGGGT GCTGCGCGGC TGGGAGTTTG  12720
CTCGCAGGGC CAACCCCCCA ACCCGGGTCG GGCCCTCCGT CTCCCGAAGT TCAGACGTGT  12780
GGGCGGTTGT CGGTGTGGCG CGCGCGCCCG CGTCGCGGAG CCTGGTCTCC CCCGCGCATC  12840
```

-192-

```
CGCGCTCGCG GCTTCTTCCC GCTCCGCCGT TCCCGCCCTC GCCCGTGCAC CCCGGTCCTG  12900
GCCTCGCGTC GGCGCCTCCC GGACCGCTGC CTCACCAGTC TTTCTCGGTC CCGTGCCCCG  12960
TGGGAACCCA CCGCGCCCCC GTGGCGCCCG GGGGTGGGCG CGTCCGCATC TGCTCTGGTC  13020
GAGGTTGGCG GTTGAGGGTG TGCGTGCGCC GAGGTGGTGG TCGGTCCCCT GCGGCCGCGG  13080
GGTTGTCGGG GTGGCGGTCG ACGAGGGCCG GTCGGTCGCC TGCGGTGGTT GTCTGTGTGT  13140
GTTTGGGTCT TGCGCTGGGG GAGGCGGGGT CGACCGCTCA CGGGGTTGGC GCGGTCGCCC  13200
GGCGCCGCGC ACCCTCCGGC TTGTGTGGAG GGAGAGCGAG GGCGAGAACG GAGAGAGGTG  13260
GTATCCCCGG TGGCGTTGCG AGGGAGGGTT TGGCGTCCCG CGTCCGTCCG TCCCTCCCTC  13320
CCTCGGTGGG CGCCTTCGCG CCGCACGCGG CCGCTAGGGG CGGTCGGGGC CCGTGGCCCC  13380
CGTGGCTCTT CTTCGTCTCC GCTTCTCCTT CACCCGGGCG GTACCCGCTC CGGCGCCGGC  13440
CCGCGGGACG CCGCGGCGTC CGTGCGCCGA TGCGAGTCAC CCCCGGGTGT TGCGAGTTCG  13500
GGGAGGGAGA GGGCCTCGCT GACCCGTTGC GTCCCGGCTT CCCTGGGGGG GACCCGGCGT  13560
CTGTGGGCTG TGCGTCCCGG GGGTTGCGTG TGAGTAAGAT CCTCCACCCC CGCCGCCCTC  13620
CCCTCCCGCC GGCCTCTCGG GGACCCCTG AGACGGTTCG CCGGCTCGTC CTCCCGTGCC  13680
GCCGGGTGCC GTCTCTTTCC CGCCCGCCTC CTCGCTCTCT TCTTCCCGCG GCTGGGCGCG  13740
TGTCCCCCCT TTCTGACCGC GACCTCAGAT CAGACGTGGC GACCCGCTGA ATTTAAGCAT  13800
ATTAGTCAGC GGAGGAAAAG AAACTAACCA GGATTCCCTC AGTAACGACG AGTGAACAGG  13860
GAAGAGCCCA GCGCCGAATC CCCGCCGCGC GTCGCGGCGT GGGAAATGTG GCGTACGGAA  13920
GACCCACTCC CCGGCGCCGC TCGTGGGGGG CCCAAGTCCT TCTGATCGAG GCCCAGCCCG  13980
TGGACGGTGT GAGGCCGGTA GCGGCCCCGG CGCGCCGGGC TCGGGTCTTC CCGGAGTCGG  14040
GTTGCTTGGG AATGCAGCCC AAAGCGGGTG GTAAACTCCA TCTAAGGCTA AATACCGGCA  14100
CGAGACCGAT AGTCAACAAG TACCGTAAGG GAAAGTTGAA AAGAACTTTG AAGAGAGAGT  14160
TCAAGAGGGC GTGAAACCGT TAAGAGGTAA ACGGGTGGGG TCCGCGCAGT CCGCCCGGAG  14220
GATTCAACCC GGCGGCGCGC GTCCGGCCGT GCCCGGTGGT CCCGGCGGAT CTTTCCCGCT  14280
CCCCGTTCCT CCCGACCCCT CCACCCGCGC GTCGTTCCCC TCTTCCTCCC CGCGTCCGGC  14340
GCCTCCGGCG GCGGGCGCGG GGGGTGGTGT GGTGGTGGCG CGCGGGCGGG GCCGGGGGTG  14400
GGGTCGGCGG GGGACCGCCC CCGGCCGGCG ACCGGCCGCC GCCGGGCGCA CTTCCACCGT  14460
GGCGGTGCGC CGCGACCGGC TCCGGGACGG CCGGGAAGGC CCGGTGGGGA AGGTGGCTCG  14520
GGGGGGGCGG CGCGTCTCAG GGCGCGCCGA ACCACCTCAC CCCGAGTGTT ACAGCCCTCC  14580
GGCCGCGCTT TCGCCGAATC CCGGGGCCGA GGAAGCCAGA TACCCGTCGC CGCGCTCTCC  14640
CTCTCCCCCC GTCCGCCTCC CGGGCGGGCG TGGGGGTGGG GGCCGGGCCG CCCCTCCCAC  14700
GGCGCGACCG CTCTCCCACC CCCCTCCGTC GCCTCTCTCG GGGCCCGGTG GGGGGCGGGG  14760
CGGACTGTCC CCAGTGCGCC CCGGGCGTCG TCGCGCCGTC GGGTCCCGGG GGGACCGTCG  14820
GTCACGCGTC TCCCGACGAA GCCGAGCGCA CGGGGTCGGC GGCGATGTCG GCTACCCACC  14880
CGACCCGTCT TGAAACACGG ACCAAGGAGT CTAACGCGTG CGCGAGTCAG GGGCTCGTCC  14940
GAAAGCCGCC GTGGCGCAAT GAAGGTGAAG GGCCCCGCCC GGGGGCCCGA GGTGGGATCC  15000
CGAGGCCTCT CCAGTCCGCC GAGGGCGCAC CACCGGCCCG TCTCGCCCGC CGCGCCGGGG  15060
AGGTGGAGCA CGAGCGTACG CGTTAGGACC CGAAAGATGG TGAACTATGC TTGGGCAGGG  15120
CGAAGCCAGA GGAAACTCTG GTGGAGGTCC GTAGCGGTCC TGACGTGCAA ATCGGTCGTC  15180
CGACCTGGGT ATAGGGGCGA AAGACTAATC GAACCATCTA GTAGCTGGTT CCCTCCGAAG  15240
TTTCCCTCAG GATAGCTGGC GCTCTCGCTC CCGACGTACG CAGTTTTATC CGGTAAAGCG  15300
AATGATTAGA GGTCTTGGGG CCGAAACGAT CTCAACCTAT TCTCAAACTT TAAATGGGTA  15360
AGAAGCCCGG CTCGCTGGCG TGGAGCCGGG CGTGGAATGC GAGTGCCTAG TGGGCCACTT  15420
TTGGTAAGCA GAACTGGCGC TGCGGGATGA ACCGAACGCC GGGTTAAGGC GCCCGATGCC  15480
GACGCTCATC AGACCCCAGA AAAGGTGTTG GTTGATATAG ACAGCAGGAC GGTGGCCATG  15540
GAAGTCGGAA TCCGCTAAGG AGTGTGTAAC AACTCACCTG CCGAATCAAC TAGCCCTGAA  15600
AATGGATGGC GCTGGAGCGT CGGGCCCATA CCCGGCCGTC GCCGCAGTCG GAACGGAACG  15660
GGACGGGAGC GGCCGCGGGT GCGCGTCTCT CGGGGTCGGG GGTGCGTGGC GGGGGCCCGT  15720
CCCCCGCCTC CCCTCCGCGC GCCGGGTTCG CCCCCGCGGC GTCGGGCCCC GCGGAGCCTA  15780
CGCCGCGACG AGTAGGAGGG CCGCTGCGGT GAGCCTTGAA GCCTAGGGCG CGGGCCCGGG  15840
TGGAGCCGCC GCAGGTGCAG ATCTTGGTGG TAGTAGCAAA TATTCAAACG AGAACTTTGA  15900
AGGCCGAAGT GGAGAAGGGT TCCATGTGAA CAGCAGTTGA ACATGGGTCA GTCGGTCCTG  15960
AGAGATGGGC GAGTGCCGTT CCGAAGGGAC GGGCGATGGC CTCCGTTGCC CTCGGCCGAT  16020
CGAAAGGGAG TCGGGTTCAG ATCCCCGAAT CCGGAGTGGC GGAGATGGGC GCCGCGAGGC  16080
CAGTGCGGTA ACGCGACCGA TCCCGGAGAA GCCGGCGGGA GGCCTCGGGG AGAGTTCTCT  16140
TTTCTTTGTG AAGGGCAGGG CGCCCTGGAA TGGGTTCGCC CCGAGAGAGG GGCCCGTGCC  16200
TTGGAAAGCG TCGCGGTTCC GGCGGCGTCC GGTGAGCTCT CGCTGGCCCT TGAAAATCCG  16260
GGGGAGAGGG TGTAAATCTC GCGCCGGGCC GTACCATAT CCGCAGCAGG TCTCCAAGGT  16320
GAACAGCCTC TGGCATGTTG GAACAATGTA GGTAAGGGAA GTCGGCAAGC CGGATCCGTA  16380
ACTTCGGGAT AAGGATTGGC TCTAAGGGCT GGGTCGGTCG GCTGGGGCG CGAAGCGGGG  16440
CTGGGCGCGC GCCGCGGCTG GACGAGGCGC CGCCGCCCTC TCCCACGTCC GGGGAGACCC  16500
CCCGTCCTTT CCGCCCGGGC CCGCCCTCCC CTCTTCCCCG CGGGGCCCCG TCGTCCCCCG  16560
CGTCGTCGCC ACCTCTCTTC CCCCTCCTT CTTCCCGTCG GGGGCGGGT CGGGGGTCGG  16620
CGCGCGGCGC GGGCTCCGGG GCGGCGGGTC CAACCCCGCG GGGGTTCCGG AGCGGGAGGA  16680
ACCAGCGGTC CCCGGTGGGG CGGGGGGCCC GGACACTCGG GGGGCCGGCG GCGGCGGCGA  16740
CTCTGGACGC GAGCCGGGCC CTTCCCGTGG ATCGCCTCAG CTGCGGCGGG CGTCGCGGCC  16800
GCTCCCGGGG AGCCCGGCGG GTGCCGGCGC GGGTCCCCTC CCCGCGGGGC CTCGCTCCAC  16860
```

-193-

```
CCCCCCATCG CCTCTCCCGA GGTGCGTGGC GGGGGCGGGC GGGCGTGTCC CGCGCGTGTG 16920
GGGGGAACCT CCGCGTCGGT GTTCCCCCGC CGGGTCCGCC CCCCGGGCCG CGGTTTTCCG 16980
CGCGGCGCCC CCGCCTCGGC CGGCGCCTAG CAGCCGACTT AGAACTGGTG CGGACCAGGG 17040
GAATCCGACT GTTTAATTAA AACAAAGCAT CGCGAAGGCC CGCGGCGGGT GTTGACGCGA 17100
TGTGATTTCT GCCCAGTGCT CTGAATGTCA AAGTGAAGAA ATTCAATGAA GCGCGGGTAA 17160
ACGGCGGGAG TAACTATGAC TCTCTTAAGG TAGCCAAATG CCTCGTCATC TAATTAGTGA 17220
CGCGCATGAA TGGATGAACG AGATTCCCAC TGTCCCTACC TACTATCCAG CGAAACCACA 17280
GCCAAGGGAA CGGGCTTGGC GGAATCAGCG GGGAAAGAAG ACCCTGTTGA GCTTGACTCT 17340
AGTCTGGCAC GGTGAAGAGA CATGAGAGGT GTAGAATAAG TGGGAGGCCC CCGGCGCCCG 17400
GCCCCGTCCT CGCGTCGGGG TCGGGGCACG CCGGCCTCGC GGGCCGCCGG TGAAATACCA 17460
CTACTCTCAT CGTTTTTTCA CTGACCCGGT GAGGCGGGGG GGCGAGCCCC GAGGGGCTCT 17520
CGCTTCTGGC GCCAAGCGTC CGTCCCGCGC GTGCGGGCGG CGCGACCCG CTCCGGGGAC 17580
AGTGCCAGGT GGGGAGTTTG ACTGGGGCGG TACACCTGTC AAACGGTAAC GCAGGTGTCC 17640
TAAGGCGAGC TCAGGGAGGA CAGAAACCTC CCGTGGAGCA GAAGGGCAAA AGCTCGCTTG 17700
ATCTTGATTT TCAGTACGAA TACAGACCGT GAAAGCGGGG CCTCACGATC CTTCTGACCT 17760
TTTGGGTTTT AAGCAGGAGG TGTCAGAAAA GTTACCACAG GGATAACTGG CTTGTGGCGG 17820
CCAAGCGTTC ATAGCGACGT CGCTTTTTGA TCCTTCGATG TCGGCTCTTC CTATCATTGT 17880
GAAGCAGAAT TCACCAAGCG TTGGATTGTT CACCCACTAA TAGGGAACGT GAGCTGGGTT 17940
TAGACCGTCG TGAGACAGGT TAGTTTTACC CTACTGATGA TGTGTTGTTG CCATGGTAAT 18000
CCTGCTCAGT ACGAGAGGAA CCGCAGGTTC AGACATTTGG TGTATGTGCT TGGCTGAGGA 18060
GCCAATGGGG CGAAGCTACC ATCTGTGGGA TTATGACTGA ACGCCTCTAA GTCAGAATCC 18120
GCCCAAGCGG AACGATACGG CAGCGCCGAA GGAGCCTCGG TTGGCCCCGG ATAGCCGGGT 18180
CCCCGTCCGT CCCGCTCGGC GGGGTCCCCG CGTCGCCCCG CGGCGGCGCG GGGTCTCCCC 18240
CCGCCGGGCG TCGGGACCGG GGTCCGGTGC GGAGAGCCGT TCGTCTTGGG AAACGGGGTG 18300
CGGCCGGAAA GGGGGCCGCC CTCTCGCCCG TCACGTTGAA CGCACGTTCG TGTGGAACCT 18360
GGCGCTAAAC CATTCGTAGA CGACCTGCTT CTGGGTCGGG GTTTCGTACG TAGCAGAGCA 18420
GCTCCCTCGC TGCGATCTAT TGAAAGTCAG CCCTCGCACA AAGGGTTTGT CTCTGCGGGC 18480
TTTCCCGTCG CACGCCCGCT CGCTCGCACG CGACCGTGTC GCCGCCCGGG CGTCACGGGG 18540
GCGGTCGCCT CGGCCCCCGC GCGGTTGCCC GAACGACCGT GTGGTGGTTG GGGGGGGGAT 18600
CGTCTTCTCC TCCGTCTCCC GAGGACGGTT CGTTTCTCTT TCCCCTTCCG TCGCTCTCCT 18660
TGGGTGTGGG AGCCTCGTGC CGTCGCGACC GCGGCCTGCC GTCGCCTGCC GCCGCAGCCC 18720
CTTGCCCTCC GGCCTTGGCC AAGCCGGAGG GCGGAGGAGG GGGATCGGCG GCGGCGGCGA 18780
CCGCGGCGCG GTGACGCACG GTGGGATCCC CATCCTCGGC GCGTCCGTCG GGGACGGCCG 18840
GTTGGAGGGG CGGGAGGGGT TTTTCCCGTG AACGCCGCGT TCGGCGCCAG GCCTCTGGCG 18900
GCCGGGGGGG CGCTCTCTCC GCCCGAGCAT CCCCACTCCC GCCCCTCCTC TTCGCGCGCC 18960
GCGGCGGCGA CGTGCGTACG AGGGGAGGAT GTCGCGGTGT GGAGGCGGAG AGGGTCCGGC 19020
GCGGCGCCTC TTCCATTTTT TCCCCCCCAA CTTCGGAGGT CGACCAGTAC TCCGGGCGAC 19080
ACTTTGTTTT TTTTTTTTCC CCCGATGCTG GAGGTCGACC AGATGTCCGA AAGTGTCCCC 19140
CCCCCCCCCC CCCCCGGCG CGGAGCGGCG GGGCCACTCT GGACTCTTTT TTTTTTTTTT 19200
TTTTTTTTTT TTAAATTCCT GGAACCTTTA GGTCGACCAG TTGTCCGTCT TTTACTCCTT 19260
CATATAGGTC GACCAGTACT CCGGGTGGTA CTTTGTCTTT TTCTGAAAAT CCCAGAGGTC 19320
GACCAGATAT CCGAAAGTCC TCTCTTTCCC TTTACTCTTC CCCACAGCGA TTCTCTTTTT 19380
TTTTTTTTTT TTTGGTGTGC CTCTTTTTGA CTTATATACA TGTAAATAGT GTGTACGTTT 19440
ATATACTTAT AGGAGGAGGT CGACCAGTAC TCCGGGCGAC ACTTTGTTTT TTTTTTTTTT 19500
TCCACCGATG ATGGAGGTCG ACCAGATGTC CGAAAGTGTC CCGTCCCCCC CCTCCCCCCC 19560
CCGCGACGCG GCGGGCTCAC TCTGGACTCT TTTTTTTTTT TTTTTTTTTT TTTAAATTTC 19620
TGGAACCTTA AGGTCGACCA GTTGTCCGTC TTTCACTCAT TCATATAGGT CGACCGGTGG 19680
TACTTTGTCT TTTTCTGAAA ATCGCAGAGG TCGACCAGAT GTCAGAAAGT CTGGTGGTCG 19740
ATAAATTATC TGATCTAGAT TTGTTTTTCT GTTTTTCAGT TTTGTGTTGT TTTGTGTTGT 19800
TTTGTGTTGT TTTGTTTTGT TTTGTTTTGT TTTGTTTTGT TTTGTTTTGT TTTGTTTTGT 19860
TTTGTGTTGT GTTGTGTTGT GTTGTGTTGG GTTGGGTTGG GTTGGGTTGG GTTGGGTTGG 19920
GTTGGGTTGG GTTGGGTTGT GTTGTTTGGT TTTGTGTTGT TTGGTGTTGT TGGTTTTGTT 19980
TTGTTTGCTG TTGTTTTGTG TTTTGCGGGT CGAACAGTTG TCCCTAACCG AGTTTTTTTG 20040
TACACAAACA TGCACTTTTT TTAAAATAAA TTTTTAAAAT AAATGCGAAA ATCGACCAAT 20100
TATCCCTTTC CTTCTCTCTC TTTTTAAAA ATTTTCTTTG TGTGTGTGTG TGTGTGTGTG 20160
TGTGTGTGTG TGCGTGTGTG TGTGTGTGTG CGTGCAGCGT GCGCGCGCTC GTTTTATAAA 20220
TACTTATAAT AATAGGTCGC CGGGTGGTGG TAGCTTCCCG GACTCCAGAG GCAGAGGCAG 20280
GCAGACTTCT GAGTTCGAGG CCAGCCTGGT CTACAGAGGA ACCCTGTCTC GAAAAATGAA 20340
AATAAATACA TACATACATA CATACATACA TACATACATA CATACATACA TACATATGAG 20400
GTTGACCAGT TGTCAATCCT TTAGAATTTT GTTTTAATT AATGTGATAG AGAGATAGAT 20460
AATAGATAGA TGGATAGAGT GATACAAATA TAGGTTTTTT TTTCAGTAAA TATGAGGTTG 20520
ATTAACCACT TTTCCCTTTT TAGGTTTTTT TTTTTTCCC CTGTCCATGT GGTTGCTGGG 20580
ATTTGAACTC AGGACCCTGG CAGGTCAACT GGAAAACGTG TTTTCTATAT ATATAAATAG 20640
TGGTCTGTCT GCTGTTTGTT TGTTTGCTTG CTTGCTTGCT TGCTTGCTTG CTTGCTTGCT 20700
TGCTTTTTTT TTTCTTCTGA GACAGTATTT CTCTGTGTAA CCTGGTGCCC TGAAACTCAC 20760
TCTGTAGACC AGCCTGGCCT CAATCGAACT CAGAAATCCT CCTGCCTCTT GTCTACCTCC 20820
CAATTTTGGA GTAAAGGTGT GCTACACCAC TGCCTGGCAT TATTATCATT ATCATTATTA 20880
```

```
ATTTTATTAT TAGACAGAAC GAAATCAACT AGTTGGTCCT GTTTCGTTAA TTCATTTGAA    20940
ATTAGTTGGA CCAATTAGTT GGCTGGTTTG GGAGGTTTCT TTTGTTTCCG ATTTGGGTGT    21000
TTGTGGGGCT GGGGATCAGG TATCTCAACG GAATGCATGA AGGTTAAGGT GAGATGGCTC    21060
GATTTTTGTA AAGATTACTT TTCTTAGTCT GAGGAAAAAA TAAAATAATA TTGGGCTACG    21120
TTTCATTGCT TCATTTCTAT TTCTCTTTCT TTCTTTCTTT CTTTCAGATA AGGAGGTCGG    21180
CCAGTTCCTC CTGCCTTCTG GAAGATGTAG GCATTGCATT GGGAAAAGCA TTGTTTGAGA    21240
GATGTGCTAG TGAACCAGAG AGTTTGGATG TCAAGCCGTA TAATGTTTAT TACAATATAG    21300
AAAAGTTCTA ACAAAGTGAT CTTTAACTTT TTTTTTTTTT TTTCTCCTTC TACTTCTACT    21360
TGTTCTCACT CTGCCACCAA CGCGCTTTGT ACATTGAATG TGAGCTTTGT TTTGCTTAAC    21420
AGACATATAT TTTTTCTTTT GGTTTTGCTT GACATGGTTT CCCTTTCTAT CCGTGCAGGG    21480
TTCCCAGACG GCCTTTTGAG AATAAAATGG GAGGCCAGAA CCAAAGTCTT TTGAATAAAG    21540
CACCACAACT CTAACCTGTT TGGCTGTTTT CCTTCCCAAG GCACAGATCT TTCCCAGCAT    21600
GGAAAAGCAT GTAGCAGTTG TAGGACACAC TAGACGAGAG CACCAGATCT CATTGTGGGT    21660
GGTTGTGAAC CACCCACCAT GTGGTTGCCT GGGATTTGAA CTCAGGATCT TCAGAAGACG    21720
AGTCAGGGCT CTAAACCGAT GAGCCATCTC TCCAGCCCTC CTACATTCCT TCTTAAGGCA    21780
TGAATGATCC CAGCATGGGA AGACAGTCTG CCCTCTTTGT GGTATATCAC CATATACTCA    21840
ATAAAATAAT GAAATGAATG AAGTCTCCAC GTATTTATTT CTTCGAGCTA TCTAAATTCT    21900
CTCACAGCAC CTCCCCCTCC CCCACACTGC CTTTCTCCCT ATGTTTGGGT GGGGCTGGGG    21960
GAGGGGTGGG GTGGGGGCAG GGATCTGCAT GTCTTCTTGC AGGTCTGTGA ACTATTTGCG    22020
ATGGCCTGGT TCTCTGAACT GTTGAGCCTT GTCTATCCAG AGGCTGACTG GCTAGTTTTC    22080
TACCTGAAGT CCCTGAGTGA TGATTCCCT GTGAATTC                             22118
```

    (2) INFORMATION FOR SEQ ID NO:17:

         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 42999 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: Genomic DNA
       (iii) HYPOTHETICAL: NO
        (iv) ANTI-SENSE: NO
         (v) FRAGMENT TYPE:
        (vi) ORIGINAL SOURCE:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GCTGACACGC TGTCCTCTGG CGACCTGTCG TCGGAGAGGT TGGGCCTCCG GATGCGCGCG      60
GGGCTCTGGC CTCACGGTGA CCGGCTAGCC GGCCGCGCTC CTGCCTTGAG CCGCCTGCCG     120
CGGCCCGCGG GCCTGCTGTT CTCTCGCGCG TCCGAGCGTC CCGACTCCCG GTGCCGGCCC     180
GGGTCCGGGT CTCTGACCCA CCCGGGGGCG GCGGGGAAGG CGGCGAGGGC CACCGTGCCC     240
CGTGCGCTCT CCGCTGCGGG CGCCCGGGGC GCCGCACAAC CCCACCCGCT GGCTCCGTGC     300
CGTGCGTGTC AGGCGTTCTC GTCTCCGCGG GGTTGTCCGC CGCCCCTTCC CCGGAGTGGG     360
GGGTGGCCGG AGCCGATCGG CTCGCTGGCC GGCCGGCCTC CGCTCCCGGG GGGCTCTTCG     420
ATCGATGTGG TGACGTCGTG CTCTCCCGGG CCGGGTCCGA GCCGCGAAGC GCGAGGGGCG     480
GACGTTCGTG GCGAACGGGA CCGTCCTTCT CGCTCCGCCC GCGCGGTCCC CTCGTCTGCT     540
CCTCTCCCCG CCCGCCGGCC GGCGTGTGGG AAGGCGTGGG GTGCGGACCC CGGCCCGACC     600
TCGCCGTCCC GCCCGCCGCC TTCGCTTCGC GGGTGCGGGC CGGCGGGGTC CTCTGACGCG     660
GCAGACAGCC CTGCCTGTCG CCTCCAGTGG TTGTCGACTT GCGGGCGGCC CCCCTCCGCG     720
GCGGTGGGGG TGCCGTCCCG CCGGCCCGTC GTGCTGCCCT CTCGGGGGGG GTTTGCGCGA     780
GCGTCGGCTC CGCCTGGGCC CTTGCGGTGC TCCTGGAGCG CTCCGGGTTG TCCCTCAGGT     840
GCCCGAGGCC GAACGGTGGT GTGTCGTTCC CGCCCCCGGC GCCCCCTCCT CCGGTCGCCG     900
CCGCGGTGTC CGCGCGTGGG TCCTGAGGGA GCTCGTCGGT GTGGGGTTCG AGGCGGTTTG     960
AGTGAGACGA GACGAGACGC GCCCCTCCCA CGCGGGGAAG GGCGCCCGCC TGCTCTCGGT    1020
GAGCGCACGT CCCGTGCTCC CCTCTGGCGG GTGCGGCGGG GCCGTGTGAG CGATCGCGGT    1080
GGGTTCGGGC CGGTGTGACG CGTGCGCCGG CCGGCCGCCG AGGGGCTGCC GTTCTGCCTC    1140
CGACCGGTCG TGTGTGGGTT GACTTCGGAG GCGCTCTGCC TCGGAAGGAA GGAGGTGGGT    1200
GGACGGGGGG GCCTGGTGGG GTTGCGCGCA CGCGCGCACC GGCCGGGCCC CCGCCCTGAA    1260
CGCGAACGCT CGAGGTGGCC GCGCGCAGGT GTTTCCTCGT ACCGCAGGGC CCCCTCCCTT    1320
CCCCAGGCGT CCCTCGGCGC CTCTGCGGGC CCGAGGAGGA GCGGCTGGCG GGTGGGGGGA    1380
GTGTGACCCA CCCTCGGTGA GAAAAGCCTT CTCTAGCGAT CTGAGAGGCG TGCCTTGGGG    1440
GTACCGGATC CCCCGGGCCG CCGCCTCTGT CTCTGCCTCC GTTATGGTAG CGCTGCCGTA    1500
GCGACCCGCT CGCAGAGGAC CCTCCTCCGC TTCCCCCTCG ACGGGGTTGG GGGGGAGAAG    1560
CGAGGGTTCC GCCGGCCACC GCGGTGGTGG CCGAGTGCGG CTCGTCGCCT ACTGTGGCCC    1620
GCGCCTCCCC CTTCCGAGTC GGGGGAGGAT CCCGCCGGGC CGGGCCCGGC GCTCCCACCC    1680
AGCGGGTTGG GACGCGGCGG CCGGCGGGCG GTGGGTGTGC GCGCCCGGCG CTCTGTCCGG    1740
```

```
CGCGTGACCC CCTCCGTCCG CGAGTCGGCT CTCCGCCCGC TCCCGTGCCG AGTCGTGACC    1800
GGTGCCGACG ACCGCGTTTG CGTGGCACGG GGTCGGGCCC GCCTGGCCCT GGGAAAGCGT    1860
CCCACGGTGG GGGCGCGCCG GTCTCCCGGA GCGGGACCGG GTCGGAGGAT GGACGAGAAT    1920
CACGAGCGAC GGTGGTGGTG GCGTGTCGGG TTCGTGGCTG CGGTCGCTCC GGGGCCCCCG    1980
GTGGCGGGGC CCCGGGGCTC GCGAGGCGGT TCTCGGTGGG GGCCGAGGGC CGTCCGGCGT    2040
CCCAGGCGGG GCGCCGCGGG ACCGCCCTCG TGTCTGTGGC GGTGGGATCC CGCGGCCGTG    2100
TTTTCCTGGT GGCCCGGCCG TGCCTGAGGT TTCTGTCCCGA GCCGCCGCCT CTGCCGGGCTC   2160
CCGGGTGCCC TTGCCCTCGC GGTCCCCGGC CCTCGCCCGT CTGTGCCCTC TTCCCCGCCC    2220
GCCGCCCGCC GATCCTCTTC TTCCCCCCGA GCGGCTCACC GGCTTCACGT CCGTTGGTGG    2280
CCCCGCCTGG GACCGAACCC GGCACCGCCT CGTGGGGCGC CGCCGCCGGC CACTGATCGG    2340
CCCGGCGTCC GCGTCCCCCG GCGCGCGCCT TGGGGACCGG GTCGGTGGCG CGCCGCGTGG    2400
GGCCCGGTGG GCTTCCCGGA GGGTTCCGGG GGTCGGCCTG CGGCGCGTGC GGGGGAGGAG    2460
ACGGTTCCGG GGGACCGGCC GCGGCTGCGG CGGCGGCGGT GGTGGGGGGA GCCGCGGGGA    2520
TCGCCGAGGG CCGGTCGGCC GCCCGGGTG CCCCGCGGTG CCGCCGGCGG CGGTGAGGCC     2580
CCGCGCGTGT GTCCCGGCTG CGGTCGGCCG CGCTCGAGGG GTCCCCGTGG CGTCCCCTTC    2640
CCCGCCGGCC GCCTTTCTCG CGCCTTCCCC GTCGCCCCGG CCTCGCCCGT GGTCTCTCGT    2700
CTTCTCCCGG CCCGCTCTTC CGAACCGGGT CGGCGCGTCC CCCGGGTGCG CCTCGCTTCC    2760
CGGGCCTGCC GCGGCCCTTC CCCGAGGCGT CCGTCCCGGG CGTCGGCGTC GGGGAGAGCC    2820
CGTCCTCCCC GCGTGGCGTC GCCCCGTTCG GCGCGCGCGT GCGCCCGAGC GCGGCCCGGT    2880
GGTCCCTCCC GGACAGGCGT TCGTGCGACG TGTGGCGTGG GTCGACCTCC GCCTTGCCGG    2940
TCGCTCGCCC TCTCCCCGGG TCGGGGGGTG GGGCCCGGGC CGGGGCCTCG GCCCCGGTCG    3000
CTGCCTCCCG TCCCGGGCGG GGGCGGGCGC GCCGGCCGGC CTCGGTCGCC CTCCCTTGGC    3060
CGTCGTGTGG CGTGTGCCAC CCCTGCGCCG GCGCCCGCCG GCGGGGCTCG GAGCCGGGCT    3120
TCGGCCGGGC CCCGGGCCCT CGACCGGACC GGCTGCGCGG GCGCTGCGGC CGCACGGCGC    3180
GACTGTCCCC GGGCCGGGCA CCGCGGTCCG CCTCTCGCTC GCCGCCCGGA CGTCGGGGCC    3240
GCCCCGCGGG GCGGGCGGAG CGCCGTCCCC GCCTCGCCGC CGCCCGCGGG CGCCGGCCGC    3300
GCGCGCGCGC GCGTGGCCGC CGGTCCCTCC CGGCCGCCGG GCGCGGGTCG GGCCGTCCGC    3360
CTCCTCGCGG GCGGGCGCGA CGAAGAAGCG TCGCGGGTCT GTGGCGCGGG GCCCCCGGTG    3420
GTCGTGTCGC GTGGGGGGCG GGTGGTTGGG GCGTCCGGTT CGCCGCGCCC CGCCCCGGCC    3480
CCACCGGTCC CGGCCGCCGC CCCCGCGCCC GCTCGCTCCC TCCCGTCCGC CCGTCCGCGG    3540
CCCGTCCGTC CGTCCGTCCG TCGTCCTCCT CGCTTGCGGG GCGCCGGGCC CGTCCTCGCG    3600
AGGCCCCCCG GCCGGCCGTC CGGCCGCGTC GGGGGCTCGC CGCGCTCTAC CTTACCTACC    3660
TGGTTGATCC TGCCAGTAGC ATATGCTTGT CTCAAAGATT AAGCCATGCA TGTCTAAGTA    3720
CGCACGGCCG GTACAGTGAA ACTGCGAATG GCTCATTAAA TCAGTTATGG TTCCTTTGGT    3780
CGCTCGCTCC TCTCCTACTT GGATAACTGT GGTAATTCTA GAGCTAATAC ATGCCGACGG    3840
GCGCTGACCC CCTTCGCGGG GGGGATGCGT GCATTTATCA GATCAAAACC AACCCGGTCA    3900
GCCCCTCTCC GGCCCCGGCC GGGGGGCGGG CGCCGGCGGC TTTGGTGACT CTAGATAACC    3960
TCGGGCCGAT CGCACGCCCC CCGTGGCGGC GACGACCCAT TCGAACGTCT GCCCTATCAA    4020
CTTTCGATGG TAGTCGCCGT GCCTACCATG GTGACCACGG GTGACGGGGA ATCAGGGTTC    4080
GATTCCGGAG AGGGAGCCTG AGAAACGGCT ACCACATCCA AGGAAGGCAG CAGGCGCGCA    4140
AATTACCCAC TCCCGACCCG GGGAGGTAGT GACGAAAAAT AACAATACAG GACTCTTTCG    4200
AGGCCCTGTA ATTGGAATGA GTCCACTTTA AATCCTTTAA CGAGGATCCA TTGGAGGGCA    4260
AGTCTGGTGC CAGCAGCCGC GGTAATTCCA GCTCCAATAG CGTATATTAA AGTTGCTGCA    4320
GTTAAAAAGC TCGTAGTTGG ATCTTGGGAG CGGGCGGGCG GTCCGCCGCG AGGCGAGCCA    4380
CCGCCCGTCC CCGCCCCTTG CCTCTCGGCG CCCCCTCGAT GCTCTTAGCT GAGTGTCCCG    4440
CGGGGCCCGA AGCGTTTACT TTGAAAAAAT TAGAGTGTTC AAAGCAGGCC CGAGCCGCCT    4500
GGATACCGCA GCTAGGAATA ATGGAATAGG ACCGCGGTTC TATTTTGTTG GTTTTCGGAA    4560
CTGAGGCCAT GATTAAGAGG GACGGCCGGG GGCATTCGTA TTGCGCCGCT AGAGGTGAAA    4620
TTCTTGGACC GGCGCAAGAC GGACCAGAGC GAAAGCATTT GCCAAGAATG TTTTCATTAA    4680
TCAAGAACGA AAGTCGGAGG TTCGAAGACG ATCAGATACC GTCGTAGTTC CGACCATAAA    4740
CGATGCCGAC CGGCGATGCG GCGGCGTTAT TCCCATGACC CGCCGGGCAG CTTCCGGGAA    4800
ACCAAAGTCT TTGGGTTCCG GGGGGAGTAT GGTTGCAAAG CTGAAACTTA AAGGAATTGA    4860
CGGAAGGGCA CCACCAGGAG TGGAGCCTGC GGCTTAATTT GACTCAACAC GGGAAACCTC    4920
ACCCGGCCCG GACACGGACA GGATTGACAG ATTGATAGCT CTTTCTCGAT TCCGTGGGTG    4980
GTGGTGCATG GCCGTTCTTA GTTGGTGGAG CGATTTGTCT GGTTAATTCC GATAACGAAC    5040
GAGACTCTGG CATGCTAACT AGTTACGCGA CCCCCGAGCG GTCGGCGTCC CCCAACTTCT    5100
TAGAGGGACA AGTGGCGTTC AGCCACCCGA GATTGAGCAA TAACAGGTCT GTGATGCCCT    5160
TAGATGTCCG GGGCTGCACG CGCGCTACAC TGACTGGCTC AGCGTGTGCC TACCCTACGC    5220
CGGCAGGCGC GGGTAACCCG TTGAACCCCA TTCGTGATGG GGATCGGGGA TTGCAATTAT    5280
TCCCCATGAA CGAGGGAATT CCCGAGTAAG TGCGGGTCAT AAGCTTGCGT TGATTAAGTC    5340
CCTGCCCTTT GTACACACCG CCCGTCGCTA CTACCGATTG GATGGTTTAG TGAGGCCCTC    5400
GGATCGGCCC CGCCGGGGTC GGCCCACGGC CCTGGCGGAG CGCTGAGAAG ACGGTCGAAC    5460
TTGACTATCT AGAGGAAGTA AAAGTCGTAA CAAGGTTTCC GTAGGTGAAC CTGCGGAAGG    5520
ATCATTAACG GAGCCCGGAG GGCGAGGCCC GCGGCGGCGC CGCCGCCGCC GCGCGCTTCC    5580
CTCCGCACAC CCACCCCCCC ACCGCGACGC GGCGCGTGCG CGGGCGGGGC CCGCGTGCCC    5640
GTTCGTTCGC TCGCTCGTTC GTTCGCCGCC CGGCCCCGCC GCCGCGAGAG CCGAGAACTC    5700
GGGAGGGAGA CGGGGGGGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAG AGAGAGAGAA    5760
```

```
AGAAGGGCGT GTCGTTGGTG TGCGCGTGTC GTGGGGCCGG CGGGCGGCGG GGAGCGGTCC    5820
CCGGCCGCGG CCCCGACGAC GTGGGTGTCG GCGGGCGCGG GGGCGGTTCT CGGCGGCGTC    5880
GCGGCGGGTC TGGGGGGGGTC TCGGTGCCCT CCTCCCCGCC GGGGCCCGTC GTCCGGCCCC    5940
GCCGCGCCGG CTCCCCGTCT TCGGGGCCGG CCGGATTCCC GTCGCCTCCG CCGCGCCGCT    6000
CCGCGCCGCC GGGCACGGCC CCGCTCGCTC TCCCCGGCCT TCCCGCTAGG GCGTCTCGAG    6060
GGTCGGGGGC CGGACGCCGG TCCCCTCCCC CGCCTCCTCG TCCGCCCCCC CGCCGTCCAG    6120
GTACCTAGCG CGTTCCGGCG CGGAGGTTTA AAGACCCCTT GGGGGGATCG CCCGTCCGCC    6180
CGTGGGTCGG GGGCGGTGGT GGGCCCGCGG GGGAGTCCCG TCGGGAGGGG CCCGGCCCCT    6240
CCCGCGCCTC CACCGCGGAC TCCGCTCCCC GGCCGGGGCC GCGCCGCCGC CGCCGCCGCG    6300
GCGGCCGTCG GGTGGGGGCT TTACCCGGCG GCCGTCGCGC GCCTGCCGCG CGTGTGGCGT    6360
GCGCCCCGCG CCGTGGGGGC GGGAACCCCC GGGCGCCTGT GGGGTGGTGT CCGCGCTCGC    6420
CCCCGCGTGG GCGGCGCGCG CCTCCCCGTG GTGTGAAACC TTCCGACCCC TCTCCGGAGT    6480
CCGGTCCCGT TTGCTGTCTC GTCTGGCCGG CCTGAGGCAA CCCCCTCTCC TCTTGGGCGG    6540
GGGGGGCGGG GGGACGTGCC GCGCCAGGAA GGGCCTCCTC CCGGTGCGTC GTCGGGAGCG    6600
CCCTCGCCAA ATCGACCTCG TACGACTCTT AGCGGTGGAT CACTCGGCTC GTGCGTCGAT    6660
GAAGAACGCA GCTAGCTGCG AGAATTAATG TGAATTGCAG GACACATTGA TCATCGACAC    6720
TTCGAACGCA CTTGCGGCCC CGGGTTCCTC CCGGGGCTAC GCCTGTCTGA GCGTCGCTTG    6780
CCGATCAATC GCCCCGGGGG TGCCTCCGGG CTCCTCGGGG TGCGCGGCTG GGGGTTCCCT    6840
CGCAGGGCCC GCCGGGGGCC CTCCGTCCCC CTAAGCGCAG ACCCGGCGGC GTCCGCCCTC    6900
CTCTTGCCGC CGCGCCCGCC CCTTCCCCCT CCCCCCGCGG GCCCTGCGTG GTCACGCGTC    6960
GGGTGGCGGG GGGGAGAGGG GGGCGCGCCC GGCTGAGAGA GACGGGGAGG GCGGCGCCGC    7020
CGCCGGAAGA CGGAGAGGGA AAGAGAGAGC CGGCTCGGGC CGAGTTCCCG TGGCCGCCGC    7080
CTGCGGTCCG GGTTCCTCCC TCGGGGGGCT CCCTCGCGCC GCGCGCGGCT CGGGGTTCGG    7140
GGTTCGTCGG CCCCGGCCGG GTGGAAGGTC CCGTGCCCGT CGTCGTCGTC GTCGCGCGTC    7200
GTCGGCGGTG GGGGCGTGTT GCGTGCGGTG TGGTGGTGGG GGAGGAGGAA GGCGGGTCCG    7260
GAAGGGGAAG GGTGCCGGCG GGGAGAGAGG GTCGGGGGAG CGCGTCCCGG TCGCCGCGGT    7320
TCCGCCGCCC GCCCCCGGTG GCGGCCCGAC GTCCGGCCGA CCGGCCGCTC CCCGCGCCCC    7380
TCCTCCTCCC CGCCGCCCCT CCTCCGAGGC CCCGCCCGTC CTCCTCGCCC TCCCCGCCGCG  7440
TACGCGCGCG CGCCCGCCCG CCCGGCTCGC CTCGCGGCGC GTCGGCCGGG GCCGGGAGCC    7500
CGCCCCGCCG CCCGCCCGTG GCCGCGGCGC CGGGGTTCGC GTGTCCCCGG CGGCGACCCG    7560
CGGGACGCCG CGGTGTCGTC CGCCGTCGCG CGCCCGCCTC CGGCTCGCGG CCGCGCCGCG    7620
CCGCGCCGGG GCCCCGTCCC GAGCTTCCGC GTCGGGGCGG CGCGGCTCCG CCGCCGCGTC    7680
CTCGGACCCG TCCCCCCGAC CTCCGCGGGG GAGACGCGCC GGGGCGTGCG GCGCCCGTCC    7740
CGCCCCCGGC CCGTGCCCCT CCCTCCGGTC GTCCCGCTCC GGCGGGGCGG CGCGGGGGCG    7800
CCGTCGGCCG CGCGCTCTCT CTCCCGTCGC CTCTCCCCCT CGCCGGGCCC GTCTCCCGAC    7860
GGAGCGTCGG GCGGGCGGTC GGGCCGGCGC GATTCCGTCC GTCCGTCCGC CGAGCGGCCC    7920
GTCCCCCTCC GAGACGCGAC CTCAGATCAG ACGTGGCGAC CCGCTGAATT TAAGCATATT    7980
AGTCAGCGGA GGAAAAGAAA CTAACCAGGA TTCCCTCAGT AACGGCGAGT GAACAGGGAA    8040
GAGCCCAGCG CCGAATCCCC GCCCCGCGGG GCGCGGGACA TGTGGCGTAC GGAAGACCCG    8100
CTCCCCGGCG CCGCTCGTGG GGGGCCCAAG TCCTTCTGAT CGAGGCCCAG CCCGTGGACG    8160
GTGTGAGGCC GGTAGCGGCC GGCGCGCGCC CGGGTCTTCC CGGAGTCGGG TTGCTTGGGA    8220
ATGCAGCCCA AAGCGGGTGG TAAACTCCAT CTAAGGCTAA ATACCGGCAC GAGACCGATA    8280
GTCAACAAGT ACCGTAAGGG AAAGTTGAAA AGAACTTTGA AGAGAGAGTT CAAGAGGGCG    8340
TGAAACCGTT AAGAGGTAAA CGGGTGGGGT CCGCGCAGTC CGCCCGGAGG ATTCAACCCG    8400
GCGGCGGGTC CGGCCGTGTC GGCGGCCCGG CGGATCTTTC CCGCCCCCCG TTCCTCCCGA    8460
CCCCTCCACC CGCCCTCCCT TCCCCCGCCG CCCCTCCTCC TCCTCCCCGG AGGGGGCGGG    8520
CTCCGGCGGG TGCGGGGGTG GGCGGGCGGG GCCGGGGGTG GGGTCGGCGG GGGACCGTCC    8580
CCCGACCGGC GACCGGCCGC CGCCGGGCGC ATTTCCACCG CGGCGGTGCG CCGCGACCGG    8640
CTCCGGGACG GCTGGGAAGG CCCGGCGGGG AAGGTGGCTC GGGGGGCCCC GTCCGTCCGT    8700
CCGTCCTCCT CCTCCCCCGT CTCCGCCCCC CGGCCCCGCG TCCTCCCTCG GGAGGGCGCG    8760
CGGGTCGGGG CGGCGGCGGC GGCGGCGGTG GCGGCGGCGG CGGGGGCGGC GGGACCGAAA    8820
CCCCCCCCGA GTGTTACAGC CCCCCCGGCA GCAGCACTCG CCGAATCCCG GGGCCGAGGG    8880
AGCGAGACCC GTCGCCGCGC TCTCCCCCCT CCCGGCGCCC ACCCCGCGG GGAATCCCCC    8940
GCGAGGGGGG TCTCCCCCGC GGGGGCGCGC CGGCGTCTCC TCGTGGGGGG GCCGGGCCAC    9000
CCCTCCCACG GCGCGACCGC TCTCCCACCC CTCCTCCCCG CGCCCCCGCC CCGGCGACGG    9060
GGGGGGTGCC GCGCGCGGGT CGGGGGGGCGG GGCGGACTGT CCCCAGTGCG CCCCGGGCGG    9120
GTCGCGCCGT CGGGCCCGGG GGAGGTTCTC TCGGGGCCAC GCGCGCGTCC CCCGAAGAGG    9180
GGGACGGCGG AGCGAGCGCA CGGGGTCGGC GGCGACGTCG GCTACCCACC CGACCCGTCT    9240
TGAAACACGG ACCAAGGAGT CTAACACGTG CGCGAGTCGG GGGCTCGCAC GAAAGCCGCC    9300
GTGGCGCAAT GAAGGTGAAG GCCGGCGCGC TCGCCGGCCG AGGTGGGATC CCGAGGCCTC    9360
TCCAGTCCGC CGAGGGCGCA CCACCGGCCC GTCTCGCCCG CCGCGCCGGG GAGGTGGAGC    9420
ACGAGCGCAC GTGTTAGGAC CCGAAAGATG GTGAACTATG CCTGGGCAGG GCGAAGCCAG    9480
AGGAAACTCT GGTGGAGGTC CGTAGCGGTC CTGACGTGCA AATCGGTCGT CCGACCTGGG    9540
TATAGGGGCG AAAGACTAAT CGAACCATCT AGTAGCTGGT TCCCTCCGAA GTTTCCCTCA    9600
GGATAGCTGG CGCTCTCGCA GACCCGACGC ACCCCCGCCA CGCAGTTTTA TCCGGTAAAG    9660
CGAATGATTA GAGGTCTTGG GGCCGAAACG ATCTCAACCT ATTCTCAAAC TTTAAATGGG    9720
TAAGAAGCCC GGCTCGCTGG CGTGGAGCCG GGCGTGGAAT GCGAGTGCCT AGTGGGCCAC    9780
```

-197-

```
TTTTGGTAAG CAGAACTGGC GCTGCGGGAT GAACCGAACG CCGGGTTAAG GCGCCCGATG  9840
CCGACGCTCA TCAGACCCCA GAAAAGGTGT TGGTTGATAT AGACAGCAGG ACGGTGGCCA  9900
TGGAAGTCGG AATCCGCTAA GGAGTGTGTA ACAACTCACC TGCCGAATCA ACTAGCCCTG  9960
AAAATGGATG GCGCTGGAGC GTCGGGCCCA TACCCGGCCG TCGCCGGCAG TCGAGAGTGG 10020
ACGGGAGCGG CGGGGGCGGC GCGCGCGCGC GCGCGTGTGG TGTGCGTCGG AGGGCGGCGG 10080
CGGCGGCGGC GGCGGGGTCG TGGGGTCCTT CCCCCGCCCC CCCCCCCACG CCTCCTCCCC 10140
TCCTCCCGCC CACGCCCCGC TCCCCGCCCC CGGAGCCCCG CGGACGCTAC GCCGCGACGA 10200
GTAGGAGGGC CGCTGCGGTG AGCCTTGAAG CCTAGGGCGC GGGCCCGGGT GGAGCCGCCG 10260
CAGGTGCAGA TCTTGGTGGT AGTAGCAAAT ATTCAAACGA GAACTTTGAA GGCCGAAGTG 10320
GAGAAGGGTT CCATGTGAAC AGCAGTTGAA CATGGGTCAG TCGGTCCTGA GAGATGGGCG 10380
AGCGCCGTTC CGAAGGGACG GGCGATGGCC TCCGTTGCCC TCGGCCGATC GAAAGGGAGT 10440
CGGGTTCAGA TCCCCGAATC CGGAGTGGCG GAGATGGGCG CCGCGAGGCG TCCAGTGCGG 10500
TAACGCGACC GATCCCGGAG AAGCCGGCGG GAGCCCCGGG GAGAGTTCTC TTTTCTTTGT 10560
GAAGGGCAGG GCGCCCTGGA ATGGGTTCGC CCCGAGAGAG GGGCCCGTGC CTTGGAAAGC 10620
GTCGCGGTTC CGGCGGCGTC CGGTGAGCTC TCGCTGGCCC TTGAAAATCC GGGGGAGAGG 10680
GTGTAAATCT CGCGCCGGGC CGTACCCATA TCCGCAGCAG GTCTCCAAGG TGAACAGCCT 10740
CTGGCATGTT GGAACAATGT AGGTAAGGGA AGTCGGCAAG CCGGATCCGT AACTTCGGGA 10800
TAAGGATTGG CTCTAAGGGC TGGGTCGGTC GGGCTGGGGC GCGAAGCGGG GCTGGGCGCG 10860
CGCCGCGGCT GGACGAGGCG CGCGCCCCCC CCACGCCCGG GGCACCCCCC TCGCGGCCCT 10920
CCCCCGCCCC ACCCGCGCGC GCCGCTCGCT CCCTCCCCAC CCCGCGCCCT CTCTCTCTCT 10980
CTCTCCCCCG CTCCCCGTCC TCCCCCCTCC CCGGGGGAGC GCCGCGTGGG GGCGCGGCGG 11040
GGGGAGAAGG GTCGGGGCGG CAGGGGCCGC GCGGCGGCCG CCGGGGCGGC CGGCGGGGGC 11100
AGGTCCCCGC GAGGGGGGCC CCGGGGACCC GGGGGGCCGG CGGCGGCGCG GACTCTGGAC 11160
GCGAGCCGGG CCCTTCCCGT GGATCGCCCC AGCTGCGGCG GGCGTCGCGG CCGCCCCCGG 11220
GGAGCCCGGC GGCGGCGCGG CGCGCCCCCC ACCCCACCC CACGTCTCGG TCGCGCGCGC 11280
GTCCGCTGGG GGCGGGGAGCG GTCGGGCGGC GGCGGTCGGC GGGCGGCCGG GCGGGGCGGT 11340
TCGTCCCCCC GCCCTACCCC CCCGGCCCCG TCCGCCCCCC GTTCCCCCCT CCTCCTCGGC 11400
GCGCGGCGGC GGCGGCGGCA GGCGGCGGAG GGGCCGCGGG CCGGTCCCCC CCGCCGGGTC 11460
CGCCCCCGGG GCCGCGGTTC CGCGCGCGCC TCGCCTCGGC CGGCGCCTAG CAGCCGACTT 11520
AGAACTGGTG CGGACCAGGG GAATCCGACT GTTTAATTAA AACAAAGCAT CGCGAAGGCC 11580
CGCGGCGGGT GTTGACGCGA TGTGATTTCT GCCCAGTGCT CTGAATGTCA AAGTGAAGAA 11640
ATTCAATGAA GCGCGGGTAA ACGGCGGGAG TAACTATGAC TCTCTTAAGG TAGCCAAATG 11700
CCTCGTCATC TAATTAGTGA CGCGCATGAA TGGATGAACG AGATTCCCAC TGTCCCTACC 11760
TACTATCCAG CGAAACCACA GCCAAGGGAA CGGGCTTGGC GGAATCAGCG GGGAAAGAAG 11820
ACCCTGTTGA GCTTGACTCT AGTCTGGCAC GGTGAAGAGA CATGAGAGGT GTAGAATAAG 11880
TGGGAGGCCC CCGGCGCCCC CCCGGTGTCC CCGCGAGGGG CCCGGGCGGC GGTCCGCGGC 11940
CCTGCGGGCC GCCGGTGAAA TACCACTACT CTGATCGTTT TTTCACTGAC CCGGTGAGGC 12000
GGGGGGGCGA GCCCGAGGGG CTCTCGCTTC TGGCGCCAAG CGCCCGCCCG GCCGGGCGCG 12060
ACCCGCTCCG GGGACAGTGC CAGGTGGGGA GTTTGACTGG GGCGGTACAC CTGTCAAACG 12120
GTAACGCAGG TGTCCTAAGG CGAGCTCAGG GAGGACAGAA ACCTCCCGTG GAGCAGAAGG 12180
GCAAAAGCTC GCTTGATCTT GATTTTCAGT ACGAATACAG ACCGTGAAAG CGGGGCCTCA 12240
CGATCCTTCT GACCTTTTGG GTTTTAAGCA GGAGGTGTCA GAAAAGTTAC CACAGGGATA 12300
ACTGGCTTGT GGCGGCCAAG CGTTCATAGC GACGTCGCTT TTTGATCCTT CGATGTCGGC 12360
TCTTCCTATC ATTGTGAAGC AGAATTCGCC AAGCGTTGGA TTGTTCACCC ACTAATAGGG 12420
AACGTGAGCT GGGTTTAGAC CGTCGTGAGA CAGGTTAGTT TTACCCTACT GATGATGTGT 12480
TGTTGCCATG GTAATCCTGC TCAGTACGAG AGGAACCGCA GGTTCAGACA TTTGGTGTAT 12540
GTGCTTGGCT GAGGAGCCAA TGGGGCGAAG CTACCATCTG TGGGATTATG ACTGAACGCC 12600
TCTAAGTCAG AATCCCGCCC AGGCGAACGA TACGGCAGCG CCGCGGAGCC TCGGTTGGCC 12660
TCGGATAGCC GGTCCCCCGC CTGTCCCCGC CGGCGGGCCG CCCCCCCCTC CACGCGCCCC 12720
GCCGCGGGAG GGCGCGTGCC CCGCCGCGCG CCGGGACCGG GGTCCGGTGC GGAGTGCCCT 12780
TCGTCCTGGG AAACGGGGCG CGGCCGGAAA GGCGGCCGCC CCCTCGCCCG TCACGCACCG 12840
CACGTTCGTG GGGAACCTGG CGCTAAACCA TTCGTAGACG ACCTGCTTCT GGGTCGGGGT 12900
TTCGTACGTA GCAGAGCAGC TCCCTCGCTG CGATCTATTG AAAGTCAGCC CTCGACACAA 12960
GGGTTTGTCC GCGCGCGCGT GCGTGCGGGG GGCCCGGCGG GCGTGCGCGT TCGGCGCCGT 13020
CCGTCCTTCC GTTCGTCTTC CTCCCTCCCG GCCTCTCCCG CCGACCGCGG CGTGGTGGTG 13080
GGGTGGGGGG GAGGGCGCGC GACCCCGGTC GGCCGCCCCG CTTCTTCGGT TCCCGCCTCC 13140
TCCCCGTTCA CGCCGGGGCG GCTCGTCCGC TCCGGGCCGG GACGGGGTCC GGGGGAGCGTG 13200
GTTTGGGAGC CGCGGAGGCG CCGCGCCGAG CCGGGCCCCG TGGCCCGCCG GTCCCCGTCC 13260
CGGGGGGTTGG CCGCGCGGCG CGGTGGGGGG CCACCCGGGG TCCCGGCCCT CGCGCGTCCT 13320
TCCTCCTCGC TCCTCCGCAC GGGTCGACCG ACGAACCGCG GGTGGCGGC GGCGGGCGGC 13380
GAGCCCCACG GGCGTCCCCG CACCCGGCCG ACCTCCGCTC GCGACCTCTC CTCGGTCGGG 13440
CCTCCGGGGT CGACCGCCTG CGCCCGCGGG CGTGAGACTC AGCGGCGTCT CGCCGTGTCC 13500
CGGGTCGACC GCGGCCTTCT CCACCGAGCG GCGGTGTAGG AGTGCCCGTC GGGACGAACC 13560
GCAACCGGAG CGTCCCCGTC TCGGTCGGCA CCTCCGGGGT CGACCAGCTG CCGCCCGCGA 13620
GCTCCGGACT TAGCCGGCGT CTGCACGTGT CCCGGGTCGA CCAGCAGGCG GCCGCCGGAC 13680
GCAGCGGCGC ACGCACGCGA GGGCGTCGAT TCCCCTTCGC GCGCCCGCGC CTCCACCGGC 13740
CTCGGCCCGC GGTGGAGCTG GGACCACGCG GAACTCCCTC TCCCACATTT TTTTCAGCCC 13800
```

```
CACCGCGAGT TTGCGTCCGC GGGACCTTTA AGAGGGAGTC ACTGCTGCCG TCAGCCAGTA 13860
CTGCCTCCTC CTTTTTCGCT TTTAGGTTTT GCTTGCCTTT TTTTTTTTTT TTTTTTTTTT 13920
TTTTTTCTTT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT TTCTTTCTTT CGCTTGTCTT 13980
CTTCTTGTGT TCTCTTCTTG CTCTTCCTCT GTCTGTCTCT CTCTCTCTCT CTCTCTCTGT 14040
CTCTCGCTCT CGCCCTCTCT CTCTTCTCTC TCTCTCTCTC TCTCTCTCTG TCTCTCGCTC 14100
TCGCCCTCTC TCTCTCTCTT CTCTCTGTCT CTCTCTCTCT CTCTCTCTCT CTCTCTCTCT 14160
GTCGCTCTCG CCCTCTCGCT CTCTCTCTGT CTCTGTCTGT GTCTCTCTCT CTCCCTCCCT 14220
CCCTCCCTCC CTCCCTCCCT CCCTCCCCTT CCTTGGCGCC TTCTCGGCTC TTGAGACTTA 14280
GCCGCTGTCT CGCCGTACCC CGGGTCGACC GGCGGGCCTT CTCCACCGAG CGGCGTGCCA 14340
CAGTGCCCGT CGGGACGAGC CGGACCCGCC GCGTCCCCGT CTCGGTCGGC ACCTCCGGGG 14400
TCGACCAGCT GCCGCCCGCG AGCTCCGGAC TTAGCCGGCG TCTGCACGTG TCCCGGGTCG 14460
ACCAGCAGGC GGCCGCCGGA CGCAGCGGCG CACCGACGGA GGGCGCTGAT TCCCGTTCAC 14520
GCGCCCGCGC CTCCACCGGC CTCGGCCCGC CGTGGAGCTG GGACCACGCG GAACTCCCTC 14580
TCCTACATTT TTTTCAGCCC CACCGCGAGT TTGCGTCCGC GGGACCTTTA AGAGGGAGTC 14640
ACTGCTGCCG TCAGCCAGTA CTGCCTCCTC CTTTTTCGCT TTTAGGTTTT GCTTGCCTTT 14700
TTTTTTTTTT TTTTTTTTTT TTTTTTCTTT CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT 14760
TTCTTTCTTT CTTTCGCTCT CGCTCTCTCG CTCTCTCCCT CGCTCGTTTC TTTCTTTCTC 14820
TTTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTGTCTCTC GCTCTCGCCC TCTCTCTCTC 14880
TTTCTCTCTC TCTCTGTCTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC CCTCCCTCCC 14940
TCCCCCTCCC TCCCTCTCTC CCCTTCCTTG GCGCCTTCTC GGCTCTTGAG ACTTAGCCGC 15000
TGTCTCGCCG TGTCCCGGGT CGACCGGCGG GCCTTCTCCA CCGAGCGGCG TGCCACAGTG 15060
CCCGTCGGGA CGAGCCGGAC CCGCCGCGTC CCGTCTCGG TCGGCACCTC CGGGGTCGAC 15120
CAGCTGCCGC CCGCGAGCTC CGGACTTAGC CGGCGTCTGC ACGTGTCCCG GGTCGACCAG 15180
CAGGCGGCCG CCGGACGCTG CGGCGCACCG ACGCGAGGGC GTCGATTCCG GTTCACGCGC 15240
CGGCGACCTC CACCGGCCTC GGCCCGCGGT GGAGCTGGGA CCACGCGGAA CTCCCTCTCC 15300
CACATTTTTT TCAGCCCCAC CGCGAGTTGG CGTCCGCCGG ACTTTTAAGA GGGAGTCACT 15360
GCTGCCGTCA GCCAGTAATG CTTCCTCCTT TTTTGCTTTT TGGTTTTGCC TTGCGTTTTC 15420
TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TCTCTCTCTC TCTCTCTCTC 15480
TCTCTGTCTC TCTCTCTG TCTCTCTCCC CTCCCTCCCT CCTTGGTGCC TTCTCGGCTC 15540
GCTGCTGCTG CTGCCTCTGC CTCCACGGTT CAAGCAAACA GCAAGTTTTC TATTTCGAGT 15600
AAAGACGTAA TTTCACCATT TTGGCCGGGC TGGTCTCGAA CTCCCGACCT AGTGATCCGC 15660
CCGCCTCGGC CTCCCAAAGA CTGCTGGGAG TACAGATGTG AGCCACCATG CCCGGCCGAT 15720
TCCTTCCTTT TTTCAATCTT ATTTTCTGAA CGCTGCCGTG TATGAACATA CATCTACACA 15780
CACACACACA CACACACACA CACACACACA CACACACACA CACACACCCC GTAGTGATAA 15840
AACTATGTAA ATGATATTTC CATAATTAAT ACGTTTATAT TATGTTACTT TTAATGGATG 15900
AATATGTATC GAAGCCCCAT TTCATTTACA TACACGTGTA TGTATATCCT TCCTCCCTTC 15960
CTTCATTCAT TATTTATTAA TAATTTTCGT TTATTTATTT TCTTTTCTTT TGGGGCCGGC 16020
CCGCCTGGTC TTCTGTCTCT GCGCTCTGGT GACCTCAGCC TCCCAAATAG CTGGGACTAC 16080
AGGGATCTCT TAAGCCCGGG AGGAGAGGTT AACGTGGGCT GTGATCGCAC ACTTCCACTC 16140
CAGCTTACGT GGGCTGCGGT GCGGTGGGGT GGGGTGGGGT GGGGTGGGGT GCAGAGAAAA 16200
CGATTGATTG CGATCTCAAT TGCCTTTTAG CTTCATTCAT ACCTGTTAT TTGCTCGTTT 16260
ATTCTCATGG GTTCTTCTGT GTCATTGTCA CGTTCATCGT TTGCTTGCCT GCTTGCCTGT 16320
TTATTTCCTT CCTTCCTTCC TTCCTTCCTT CCTTCCTTCC TTCCTTCCTT CCCTCCCTTA 16380
CTGGCAGGGT CTTCCTCTGT CTCTGCCGCC CAGGATCACC CCAACCTCAA CGCTTTGGAC 16440
CGACCAAACG GTCGTTCTGC CTCTGATCCC TCCCATCCCC ATTACCTGAG ACTACAGGCG 16500
CGCACCACCA CACCGGCTGA CTTTTATGTT GTTTCTCATG TTTTCCGTAG GTAGGTATGT 16560
GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTATCT 16620
ATGTATGTAC GTATGTATGT ATGTATGTGA GTGAGATGGG TTTCGGGGTT CTATCATGTT 16680
GCCCACGCTG GTCTCGAACT CCTGTCCTCA AGCAATCCGC CTGCCTGCCT CGGCCGCCCA 16740
CACTGCTGCT ATTACAGGCG TGAGACGCTG CGCCTGGCTC CTTCTACATT TGCCTGCCTG 16800
CCTGCCTGCC TGCCTGCCTA TCAATCGTCT TCTTTTTAGT ACGGATGTCG TCTCGCTTTA 16860
TTGTCCATGC TCTGGGCACA CGTGGTCTCT TTTCAAACTT CTATGATTAT TATTATTGTA 16920
GGCGTCATCT CACGTGTCGA GGTGATCTCG AACTTTTAGG CTCCAGAGAT CCTCCCGCAT 16980
CGGCCTCCCG GAGTGCTGTG ATGACACGCG TGGGCACGGT ACGCTCTGGT CGTGTTTGTC 17040
GTGGGTCGGT TCTTTCCGTT TTTAATACGG GGACTGCGAA CGAAGAAAAT TTTCAGACGC 17100
ATCTCACCGA TCCGCCTTTT CGTTCTTTCT TTTTATTCTC TTTAGACGGA GTTTCACTCT 17160
TGTCGCCCAG GGTGGAGTAC GATGGCGGCT CTCGGCTCAC CGCACCCTCC GCCTCCCAGG 17220
TTCAAGTGAT TCTCCTGCCT CAGCCTTCCC GAGTAGCTGG AATGACAGAG ATGAGCCATC 17280
GTGCCCGGCT AATTTTTCTA TTTTTAGTAC AGATGGGGTT TCTCCATCTT GGTCAGGCTG 17340
GTCTTCAACT TCCGACCGTT GGAGAATCTT AACTTTCTTG GTGGTGGTTG TTTTCCTTTT 17400
TCTTTTTTTT TCTTTTCTTT TCTTTCCTTC TCCTCCCCCC CCCACCCCCC TTGTCGTCGT 17460
CCTCCTCCTC CTCCTCCTCC TCCTCCTCCT CCTCCTCCTC CTCCTCCTCC TCTTTCATTT 17520
CTTTCAGCTG GGCTCTCCTA CTTGTGTTGC TCTGTTGCTC ACGCTGGTCT CAAACTCCTG 17580
GCCTTGACTC TTCTCCCGTC ACATCCGCCG TCTGGTTGTT GAAATGAGCA TCTCTCGTAA 17640
AATGGAAAAG ATGAAAGAAA TAAACACGAA GACGGAAAGC ACGGTGTGAA CGTTTCTCTT 17700
GCCGTCTCCC GGGGTGTACC TTGGACCCGG AAACACGGAG GGAGCTTGGC TGAGTGGGTT 17760
TTCGGTGCCG AAACCTCCCG AGGGCCTCCT TCCCTCTCCC CCTTGTCCCC GCTTCTCCGC 17820
```

```
CAGCCGAGGC TCCCACCGCC GCCCCTGGCA TTTTCCATAG GAGAGGTATG GGAGAGGACT 17880
GACACGCCTT CCAGATCTAT ATCCTGCCGG ACGTCTCTGG CTCGGCGTGC CCCACCGGCT 17940
ACCTGCCACC TTCCAGGGAG CTCTGAGGCG GATGCGACCC CCACCCCCCC GTCACGTCCC 18000
GCTACCCTCC CCCGGCTGGC CTTTGCCGGG CGACCCCAGG GGAACCGCGT TGATGCTGCT 18060
TCGGATCCTC CGGCGAAGAC TTCCACCGGA TGCCCCGGGT GGGCCGGTTG GGATCAGACT 18120
GGACCACCCC GGACCGTGCT GTTCTTGGGG GTGGGTTGAC GTACAGGGTG GACTGGCAGC 18180
CCCAGCATTG TAAAGGGTGC GTGGGTATGG AAATGTCACC TAGGATGCCC TCCTTCCCTT 18240
CGGTCTGCCT TCAGCTGCCT CAGGCGTGAA GACAACTTCC CATCGGAACC TCTTCTCTTC 18300
CCTTTCTCCA GCACACAGAT GAGACGCACG AGAGGGAGAA ACAGCTCAAT AGATACCGCT 18360
GACCTTCATT TGTGGAATCC TCAGTCATCG ACACACAAGA CAGGTGACTA GGCAGGACA 18420
CAGATCAAAC ACTATTTCCG GGTCCTCGTG GTGGGATTGG TCTCTCTCTC TCTCTCTCTC 18480
TCTCTCTCTC TCTCTCTCTC TCTCGCACGC GCACGCGCGC ACACACACAC ACAATTTCCA 18540
TATCTAGTTC ACAGAGCACA CTCACTTCCC CTTTTCACAG TACGCAGGCT GAGTAAAACG 18600
CGCCCCACCC TCCACCCGTT GGCTGACGAA ACCCCTTCTC TACAATTGAT GAAAAAGATG 18660
ATCTGGGCCG GGCACGCTAG CTCACGCCTG TCACTCCGGC ACTTTGGGAG GCCGAGGCGG 18720
GTGGATCGCT TGGGGCCGGG AGTTCGAGAC CAGGCTGGCC GACGTGGCGA AACCCCGTCT 18780
CTCTGAAAAA TAGAACGATT AGCCGGGCCT GGTGGCGTGG GCTTGGAATC ACGACCGCTC 18840
GGGAGACTGG GGCGGGCGAC TTGTTCCAAC CGGGGAGGCC GAGGCCGCGA TGAGCTGAGA 18900
TCGTGCCGTG GCGATGCGGC CTGGATGACG GAGCGAGACC CCGTCTCGAG AGAATCATGA 18960
TGTTATTATA AGATGAGTTG TGCGCGGTGA TGGCCGCCTG TAGTCGCGGC TACTCGGGAG 19020
GCTGAGACGA GGAGAAGATC ACTTGAGGCC CCACAGGTCG AGGCTTCGGT CGGCCGTGAC 19080
CCACTGTATC CTGGGCAGTC ACCGGTCAAG GAGATATGCC CCTTCCCCGT TTGCTTTTCT 19140
TTTCTTCCCT TCTCTTTTCT TCTTTTTGCT TCTCTTTTCT TTCTTTCTTT CTTTCTTTCT 19200
TTCTTTCTTT CTTTCTTTCT TTTTCTTTTT CTCTCTTCCC CTCTTTCTTT CCTGCCTTCC 19260
TGCCTTTCTT CTTTTCTTTC TTCCTCCCTT CCTCCCTTCC TTCTTTCCTC CCGCCTCAGC 19320
CTCCCAAAGT GCTGGGATGA CTGGCGGGAG GCACCATGCC TGCTTGGCCC AAAGAGACCC 19380
TCTTGGAAAG TGAGACGCAG AGAGCGCCTT CCAGTGATCT CATTGACTGA TTTAGAGACG 19440
GCATCTCGCT CCGTCACCCC GGCAGTGGTG CCGTCGTAAC TCACTCCCTG CAGCGTGGAC 19500
GCTCCTGGAC TCGAGCGATC CTTCCACCTC AGCCTCCAGA GTACAGAGCC TGGGACCGCG 19560
GGCACGCGCC ACTGTGCCCA CACCGTTTTT AATTGTTTTT TTTTCCCCCG AGACAGAGTT 19620
TCACTCTCGT GGCCTAGACT GCAGTGCGGT GGCGCGATCT TGGCTCACCG CAACCTCTGC 19680
CTCCCGGTTT CAAGCGATTC TCCTGCATCG GCCTCCTGAG TAGCCGGGAT TGCGGGCATG 19740
CGCTGCCACG TCTGGCTGAT TTCGTATTTT TAGTGGAGAC GGGGCTTCTC CATGTCGATC 19800
GGGCTGGTTT CGAACTCCCG ACCTCAGGTG ATCCGCCCTC CCCGGCCTCC GGAAGTGCTG 19860
GGATGACAGG CGTGAGCCAC CGCGCCCGCC CTTCATTTTT AAATGTTTTC CCACAGACGG 19920
GGTCTCATCA TTTCTTTGCA ACCCTCCTGC CCGGCGTCTC AAAGTGCTGG CGTGACGGGC 19980
GTGAGCCACT GCGCCTGGAC TCCGGGGAAT GACTCACGAC CACCATCGCT CTACTGATCC 20040
TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTTGA 20100
TGAATTATCT TATGATTTAT TTGTGTACTT ATTTTCAGAC GGAGTCTCGC TCTGGGCGGG 20160
GCGAGGCGAG GCGAGGCACA GCGCATCGCT TTGGAAGCCG CGGCAACGCC TTTCAAAGCC 20220
CCATTCGTAT GCACAGAGCC TTATTCCCTT CCTGGAGTTG GAGCTGATGC CTTCCGTAGC 20280
CTTGGGCTTC TCTCCATTCG GAAGCTTGAC AGGCGCAGGG CCACCCAGAG GCTGGCTGCG 20340
GCTGAGGATT AGGGGGTGTG TTGGGGCTGA AAACTGGGTC CCCTATTTTT GATACCTCAG 20400
CCGACACATC CCCCGACCGC CATCGCTTGC TCGCCCTCTG AGATCCCCCG CCTCCACCGC 20460
CTTGCAGGCT CACCTCTTAC TTTCATTTCT TCCTTTCTTG CGTTTGAGGA GGGGGTGCGG 20520
GAATGAGGGT GTGTGTGGGG AGGGGGTGCG GGGTGGGGAC GGAGGGGAGC GTCCTAAGGG 20580
TCGATTTAGT GTCATGCCTC TTTCACCACC ACCACCACCA CCGAAGATGA CAGCAAGGAT 20640
CGGCTAAATA CCGCGTGTTC TCATCTAGAA GTGGGAACTT ACAGATGACA GTTCTTGCAT 20700
GGGCAGAACG AGGGGGACCG GGGACGCGGA AGTCTGCTTG AGGGAGGAGG GGTGGAAGGA 20760
GAGACAGCTT CAGGAAGAAA ACAAAACACG AATACTGTCG GACACAGCAC TGACTACCCG 20820
GGTGATGAAA TCATCTGCAC ACTGAACACC CCCGTCACAA GTTTACCTAT GTCACAATCT 20880
TGCACATGTA TCGCTTGAAC GACAAATAAA AGTTAGGGGG GAGAAGAGAG GAGAGAGAGA 20940
GAGAGAGAGA GACAGAGAGA GACAGAGAGA GAGAGAGAGG AGGGAGAGAG GAAAACGAAA 21000
CACCACCTCC TTGACCTGAG TCAGGGGGTT TCTGGCCTTT TGGGAGAACG TTCAGCGACA 21060
ATGCAGTATT TGGGCCCGTT CTTTTTTTTT CTTCTTCTTT TCTTTCTTTT TTTTGGACT 21120
GAGTCTCTCT CGCTCTGTCA CCCAGGCTGC GGTCGCGGTG GCGCTCACTC GGCTCACTGA 21180
AACCTCTGCT TCCCGGGTTC CAGTGATTCT TCTTCGGTAG CTGGGATTAC AGGCGCACAC 21240
CATGACGGCG GGCTCATATT CCTATTTTCA GTAGAGACGG GGTTTCTCCA CGTTGGCCAC 21300
GCTGGTCTCG AACTCCTGAC CTCAAATGAT CCGCCTTCCT GGGCCTCCCA AAGTGCTGGA 21360
AACGACAGGC CTGAGCCGCC GGGATTTCAG CCTTTAAAAG CGCGGCCCTG CCACCTTTCG 21420
CTGTGGCCCT TACGCTCAGA ATGACGTGTC CTCTCTGCCG TAGGTTGACT CCTTGAGTCC 21480
CCTAGGCCAT TGCACTGTAG CCTGGGCAGC AAGAGCCAAA CTCCGNNCCC CCACCTCCTC 21540
GCGCACATAA TAACTAACTA ACAAACTAAC TAACTAACTA AACTAACTAA CTAACTAAAA 21600
TCTCTACACG TCACCCATAA GTGTGTGTTC CCGTGAGAGT GATTTCTAAG AAATGGTACT 21660
GTACACTGAA CGCAGTGGCT CACGCTGTTC ATCCCGAGGT CAGGAGTTCG AGACCAGCCC 21720
GGCCAACGTG GTGAAACCCC GTCTCTACTG AAAATACGAA ATGGAGTCAG GCGCCGTGGG 21780
GCAGGCACCT GTAACCCCAG CTACTCGGGA GGCTGGGGTG GAAGAATTGC TTGAACCTGG 21840
```

-200-

```
CAGGCGGAGG CTGCAGTGAC CCAAGATCGC ACCACTGCAC TACAGCCTGG GCGACAGAGT  21900
GAGACCCGGT CTCCAGATAA ATACGTACAT AAATAAATAC ACACATACAT ACATACATAC  21960
ATACATACAT ACATACATAC ATCCATGCAT ACAGATATAC AAGAAAGAAA AAAAGAAAAG  22020
AAAAGAAAGA GAAAATGAAA GAAAAGGCAC TGTATTGCTA CTGGGCTAGG GCCTTCTCTC  22080
TGTCTGTTTC TCTCTGTTCG TCTCTGTCTT TCTCTCTGTG TCTCTTTCTC TGTCTGTCTG  22140
TCTCTTTCTT TCTCTCTGTC TCTGTCTGTC TCTTTCTCTG TCTCTCTGCC TCTCTCTGCCTG 22200
TCTCACTGTG TCTGTCTTCT GTCTTACTCT CTTTCTCTCC CCGTCTGTCT CTCTCTCTCT  22260
CTCTCCCTCC CTGTTTGTTT CTCTCTCTCC CTCCCTGTCT GTTTCTCTCT CTCTCTTTCT  22320
GTCTGTTTCT GTCTCTCTCT GTCTGTCTAT GTCTTTCTCT GTCTGTCTCT TTCTCTGTCT  22380
GTCTGCCTCT CTCTTTCTTT TTCTGTGTCT CTCTGTCGGT CTCTCTCTCT CTGTCTGTCT  22440
GTCTGTCTCT CTCTCTCTCT CTCTGTGCCT ATCTTCTGTC TTACTCTCTT TCTCTGCCTG  22500
TCTGTCTGTC TCTCCCTCCC TTTCTGTTTC TCTCTCTCTC TCTCTCTCTC TCCCCTCTC  22560
CCTGTCTGTT TCTCTCCGTC TCTCTCTCTT TCTGTCTGTT TCTCACTGTC TCTCTCTGTC  22620
CATCTCTCTC TCTCTCTGTC TGTCTCTTTC GTTCTCTCTG TCTGTCTGTC TCTCTCTCTC  22680
TCTCTCTCTC TCTCTCTCTC TCCCTGTCTG TCTGTTTCTC TCTATCTCTC GCTGTCCATC  22740
TCTGTCTTTC TATGTCTGTC TCTTTCTCTG TCAGTCTGTC AGACACCCCC GTGCCGGGTA  22800
GGGCCCTGCC CCTTCCACGA AAGTGAGAAG CGCGTGCTTC GGTGCTTAGA GAGGCCGAGA  22860
GGAATCTAGA CAGGCGGGCC TTGCTGGGCT TCCCCACTCG GTGTATGATT TCGGGAGGTC  22920
GAGGCCGGGT CCCCGCTTGG ATGCGAGGGG CATTTTCAGA CTTTTCTCTC GGTCACGTGT  22980
GGCGTCCGTA CTTCTCCTAT TTCCCCGATA AGCTCCTCGA CTTCAACATA AACGGCGTCC  23040
TAAGGGTCGA TTTAGTGTCA TGCCTCTTTC ACCGCCACCA CCGAAGATGA AAGCAAAGAT  23100
CGGCTAAATA CCGCGTGTTC TCATCTAGAA GTGGGAACTT ACAGATGACA GTTCTTGCAT  23160
GGGCAGAACG AGGGGGACCG GGNACGCGGA AGCCTGCTTG AGGGRGGAGG GGYGGAAGGA  23220
GAGACAGCTT CAGGAAGAAA ACAAAACACG AATACTGTCG GACACAGCAC TGACTACCCG  23280
GGTGATGAAA TCATCTGCAC ACTGAACACC CCCGTCACAA GTTTACCTAT GTCACAGTCT  23340
TGCTCATGTA TGCTTGAACG ACAAATAAAA GTTCGGGGGG GAGAAGAGAG GAGAGAGAGA  23400
GAGAGACGGG GAGAGAGGGG GGAGAGGGGG GGGGAGAGAG AGAGAGAGAG AGAGAGAGAG  23460
AGAGAGAGAG AGAAAGAGAA GTAAAACCAA CCACCACCTC CTTGACCTGA GTCAGGGGGT  23520
TTCTGGCCTT TTGGGAGAAC GTTCAGCGAC AATGCAGTAT TTGGGCCCGT TCTTTTTTTC  23580
TTCTTCTTCT TTTCTTTCTT TTTTTTTGGA CTGAGTCTCT CTCGCTCTGT CACCCAGGCT  23640
GCGGTGCGGT GGCGCTCTCT CGGCTCACTG AAACCTCTGC TTCCCGGGTT CCAGTGATTC  23700
TTCTTCGGTA GCTGGGATTA CAGGTGCGCA CCATGACGGC CGGCTCATCG TTCTATTTTT  23760
AGTAGAGACG GGGTTTCTCC ACGTTGGCCA CGCTGGTCTC GAACTCCTGA CCACAAATGA  23820
TCCACCTTCC TGGGCCTCCC AAAGTGCTGG AAACGACAGG CCTGAGCCGC CGGGATTTCA  23880
GCCTTTAAAA GCGCGCGGCC CTGCCACCTT TCGCTGCGCG CCTTACGCTC AGAATGACGT  23940
GTCCTCTCTG CCATAGGTTG ACTCCTTGAG TCCCCTAGGC CATTGCACTG TAGCCTGGGC  24000
AGCAAGAGCC AAACTCCGTC CCCCCACCTC CCCGCGCACA TAATAACTAA CTAACTAACT  24060
AACTAACTAA AATCTCTACA CGTCACCCAT AAGTGTGTGT TCCCGTGAGG AGTGATTTCT  24120
AAGAAATGGT ACTGTACACT GAACGCAGGC TTCACGTCTG TCATCCCGAG GTCAGGAGTT  24180
CGAGACCAGC CCGGCCCACG TGGTGAAACC CCCGTCTCTA CTGAAAATAC GAAATGGAGT  24240
CAGGCGCCGT GGGGCAGGCA CCTGTAACCC CAGCTACTCG GGAGGCTGGG GTGGAAGAAT  24300
TGCTTGAACC TGGCAGGCGG AGGCTGCAGT GACCCAAGAT CGCACCACTG CACTACAGCC  24360
TGGGCGACAG AGTGAGACCC GGTCTCCAGA TAAATACGTA CATAAATAAA TACACACATA  24420
CATACATACA TACATACAAC ATACATACAT ACAGATATAC AAGAAAGAAA AAAAGAAAAG  24480
AAAAGAAAGA GAAAATGAAA GAAAAGGCAC TGTATTGCTA CTGGGCTAGG GCCTTCTCTC  24540
TGTCTGTTTC TCTCTGTTCG TCTCTGTCTT TCTCTCTGTG TCTCTTTCTC TGTCTGTCTG  24600
TCTGTCTGTC TGTCTGTCTC TTTCTTTCTT TCTGTCTCTG TCTTTGTCCC TCTCTCTCCC  24660
TCTCTGCCCT GTCTCACTGT GTCTGTCTTC TATCTTACTC TCTTTCTCTC CCCGTCTGTC  24720
TCTCTCTCAC TCCCTCCCTG TCTGTTTCTC TCTCTCTCTC TTTCTGTCTG TTTCTGTCTC  24780
TCTCTGTCTG CCTCTCTCTT TCTCTATCTG TCTCTTTCTC TGTCTGTCTG CCCCTCTCTT  24840
TCTTTTTCTG TGTCTCTCTG TCTGTCTCTC TCTCTCTCTG TGCCTATCTT CTGTCTTACT  24900
CTCTTTCTCT GCCTGTCTGT CTGTCTCTCT CTGTCTCTCC CTCCCTTTCT GCTTCTCTCT  24960
CTCTCTCTCT CTCTNNNCCC TCCCTGTCTG TTTCTCTCTG TCTCCCTCTC TTTCTGTCTG  25020
TTTCTCACTG TCTCTCTCTG TCTGTCTGTT TCATTCTCTC TGTCTCTGTC TCTGTCTCTC  25080
TCTCTCTCTG TCTCTCCCTC TCTGTGTGTA TCTTTTGTCT TACTCTCTCT CTCTGCCTGT  25140
CCGTCTGTCT GTCTGTCTCT CTCTCTCCCT GTCCCTCTCT CTTTCTGTCT GTTTCTCTCT  25200
CTCTCTCTCT CTCTCTCTCT CTGTCTCCGT CTTTCTCTGT CTGTCCCTTT CTCTGTCTGT  25260
CTGCCTCTCT CTTTCTCTTT CTGTGTCTCT CTGTCTCTCT CTCTGTGCCT ATCTTCTGTC  25320
TTACTCTCTT TCTCTGCCTG TCTATCTGTC TGTCTCTCTC TGTCTCTCTC CCTGCCTTTC  25380
TGTTTCTCTC TCTCTCCCTC TCTCGCTCTC TCTGTCTTTC TCTCTTTCTC TCTGTTTCTC  25440
TGTCTCTCTC TGTCCGTCTC TGTCTTTTTC TGTCTGTCTG TCTCTCTCTT TCTTTCTGTC  25500
GTCTGTCTCT GTCTCTGTCT CTGTCTCTCT CTCTCTCTCT CTCCTTGTCT CTCTCACTGT  25560
GTCTGTCTTC TGTCTTACTC TCCTTCTCTG CCTGTCCATC TGTCTGTCTG TCTCTCTCTC  25620
TCTCTCCCTA CCTTTCTGTT TCTCTCTCGC TAGCTCTCTC TCTCTCTGCC TGTTTCTCTC  25680
TTTCTCTCTC TGTCTTTCTC TGTCTGTCTC TTTCTCTGTC TGTCTGTCTC TTTCTCTCTG  25740
TCTCTGTCTC TGTCTCTCTC TCTCTCTCTC TCTCTCTCTC TGCCTCTCTC ACTGTGTCTG  25800
TCTTCTGTCT TATTCTCTTT CTCTCTCTGT CTCTCTCTCT CTCTCCTTTA CTGTCTGTTT  25860
```

-201-

```
CTCTCTCTCT CTCTCTCTTT CTGCCTGTTT CTCTCTGTCT GTCTCTGTCT TTCTCTGTCT 25920
GTCTGCCTCT CTCTTTCTTT TTCTGCGTCT CTCTGTCTCT CTCTCTCTCT CTCTGTTCCT 25980
ATCTTCTGTC TTACTCTGTT TCCTTGCCTG CCTGCCTGTC TGTGTGTCTG TCTCTCTCTC 26040
TCTCTCTCTC TCTCTCTCCC TCCCTTTCTC TTTCTCTGTC TCTCTCTCTC TTTCTGGGTG 26100
TTTCTCTCTG TCTCTCTGTC CATCTCTGTC TTTCTATGTC TGTCTCTCTC TTTCTCTCTG 26160
TCTCTGTCTC TGCCTCTCTC TCTCTCTGTC TCTCTCTCTC TCTGTCTGTC TCTCTCACTG 26220
TGTGTGTCTG TCTTCTGTCT TACTCTCCTT CTCTGCCTGT CCGTCTGTCT GTCTGTCTCT 26280
CCCTCTCTCT CCCTCCCTTT CTGTTTCTCT CTCTCTCTCT TTCTGTCTGT TTCTCTCTTT 26340
CTCTCTCTGT CTGTCTCTTT CTCTGTCTGT CTGTCTCTCT CTTTCTTTTT CTCTGTCTCT 26400
CTGTCTCTCT CTGTGTCTGT CTCTCTGTCT GTGCCTATCT TCTGTCTTAC TCTCTTTCTC 26460
TGGCTGTCTG CCTGTCTCTC TCTCTCTCTC TGTCTGTCTC CGTCCCTCTC TCCCTGTCTG 26520
TCTGTTTCTC TCTCTGCCTC TCTCTCTCTC TGTCTGTCTC TTTCTCTGTC TGTCTGTCTC 26580
TCTCTTTCTT TTTCTCTGTC TCTCTGTCTC TCTCTGTGTC TGTCTCTCTT TCTGTGCCTA 26640
TCTTCTGTCT TACTCTCTTT CTCTGGCTGT CTGCCTGTCT CTCTCTCTCT GCCTGTCTCC 26700
GTCCCTCCCT CCCTGTCTGT CTGTTTCTCT CTCTGTCTCT GTCTCTCTGT CCATCTCTGT 26760
CTGTCTCTTT CTCTTTCTCT CTCTCTGTCT CTGTCTCTGC CTGTCTCTCT 26820
CACTGTGTCT GTCTTCTGTC TTACTCTCTT TCTCTTGCCT GCCTCTCTGT CTGTCTGTCT 26880
CTCTCCCTCC ATGTCTCTCT CTCTCTCTCA CTCACTCTCT CTCCGTCTCT CTCTCTTTCT 26940
GTCTGTTTCT CTCTCTGTCT GTCTCTCTCC CTCCATGTCT CTCTCTCTCT CTCTCACTCA 27000
CTCTCTCTCC GTCTCTCTCT CTCTTTCTGT CTGTTTCTCT CTCTGTCTGT CTCTCTCCCT 27060
CCATGTCTCT CTCTCTCCCT CTCACTCACT CTCTCTCCGT CTCTCTCTCT CTTTCTGTCT 27120
GTTTCTTTGT CTGTCTGTCT GTCTGTCTGT CTGTCTCTCT CTCTCTCTCT CTCTCTCTCT 27180
CTCTCTGTTT GTCTTTCTCC CTCCCTGTCT GTCTGTCTGT CTCTCTCTCT CTGTCTCTGT 27240
CTCTGTCTCT CTCTCTTTCT CTTTCTGTCT GTTTCTCTCT ATCTCTCGCT GTCCATCTCT 27300
GTCTTTCTAT GTCTGTCTCT TTCTCTGTCA GTCTGTCAGA CACACCCGTG CCGGTAGGGC 27360
CCTGCCCTTC CACGAGAGTG AGAAGCGCGT GCTTCGGTGC TTAGAGAGGC CGAGAGGAAT 27420
CTAGACAGGC GGGCCTTGCT GGGCTTCCCC ACTCGGTGTA CGATTTCGGG AGGTCGAGGC 27480
CGGGTCCCCG CTTGGATGCG AGGGGCATTT TCAGACTTTT CTCTCGGTCA CGTGTGGCGT 27540
CCGTACTTCT CCTATTTCCC CGATAAGTCT CCTCGACTTC AACATAAACT GTTAAGGCCG 27600
GACGCCAACA CGGCGAAACC CCGTCTCTAC TAAAAATACA AAGCTGAGTC GGGAGCGGTG 27660
GGGCAGGCCC TGTAATGCCA GCTCCTCGGG AGGCTGAGGC GGGAGAATCG CTTGAACCAG 27720
GGAAGCGGAG GCTGCAGGGA GCCGAGATCG CGCCACTGCA CTACGGCCCA GGCTGTAGAG 27780
TGAGTGAGAC TCGGTCTCTA AATAAATACG GAAATTAATT AATTCATTAA TTCTTTTCCC 27840
TGCTGACGGA CATTTGCAGG CAGGCATCGG TTGTCTTCGG GCATCACCTA GCGGCCACTG 27900
TTATTGAAAG TCGACGTTGA CACGGAGGGA GGTCTCGCCG ACTTCACCGA GCCTGGGGCA 27960
ACGGGTTTCT CTCTCTCCCT TCTGGAGGCC CCTCCCTCTC TCCCTCGTTG CCTAGGGAAC 28020
CTCGCCTAGG GAACCTCCGC CCTGGGGGCC CTATTGTTCT TTGATCGGCG CTTTACTTTT 28080
CTTTGTGTTT TGGCGCCTAG ACTCTTCTAC TTGGGCTTTG GGAAGGGTCA GTTTAATTTT 28140
CAAGTTGCCC CCCGGCTCCC CCCACTACCC ACGTCCCTTC ACCTTAATTT AGTGAGNCGG 28200
TTAGGTGGGT TTCCCCCAAA CCGCCCCCCC CCCCCGCCT CCCAACACCC TGCTTGGAAA 28260
CCTTCCAGAG CCACCCCGGT GTGCCTCCGT CTTCTCTCCC CTTCCCCCAC CCCTTGCCGG 28320
CGATCTCATT CTTGCCAGGC TGACATTTGC ATCGGTGGGC GTCAGGCCTC ACTCGGGGGC 28380
CACCGTTTTT GAAGATGGGG GCGGCACGGT CCCACTTCCC CGGAGGCAGC TTGGGCCGAT 28440
GGCATAGCCC CTTGACCCGC GTGGGCAAGC GGGCGGGTCT GCAGTTGTGA GGCTTTTCCC 28500
CCCGCTGCTT CCCGCTCAGG CCTCCCTCCA TAGGAAAGCT TCACCCTGGC TGGGTCTCGG 28560
TCACCTTTTA TCACGATGTT TTAGTTTCTC CGCCCTCCGG CCAGCAGAGT TTCACAATGC 28620
GAAGGGCGCC ACGGCTCTAG TCTGGGCCTT CTCAGTACTT GCCCAAAATA GAAACGCTTT 28680
CTGAAAACTA ATAACTTTNC TCACTTAAGA TTTCCAGGGA CGGCGCCTTG GCCCGTGTTT 28740
GTTGGCTTGT TTTGTTTCGT TCTGTTTTGT TTTGTTCGTG TTTTTCCTTT CTCGTATGTC 28800
TTTCTTTTCA GGTGAAGTAG AAATCCCCAG TTTTCAGGAA GACGTCTATT TTCCCCAAGA 28860
CACGTTAGCT GCCGTTTTTT CCTGTTGTGA ACTAGCGCTT TTGTGACTCT CTCAACGCTG 28920
CAGTGAGAGC CGGTTGATGT TTACNATCCT TCATCATGAC ATCTTATTTT CTAGAAATCC 28980
GTAGGCGAAT GCTGCTGCTG CTCTTGTTGC TGTTGTTGTT GTTGTTGTTG TCGTCGTTGC 29040
TGTTGTCGTT GTCGTTGTTG TTGTCGTTGT CGTTGTTTTC AAAGTATACC CCGGCCACCG 29100
TTTATGGGAT CAAAAGCATT ATAAAATATG TGTGATTATT TCTTGAGCAC GCCCTTCCTC 29160
CCCCTCTCTC TGTCTCTCTG TCTGTCTCTG TCTCTCTCTT TCTCTGTCTG TCTTCTCTCT 29220
CTCTCTCTCT CTGTGTCTCT CTCTCTCTGC CTGTCTGTTT CTCTCTCTCT GCCTCTCTCT 29280
CTCTCTCTCT CTCTGCCTGT CTCTCTCACT GTGTCTGTCT TCTGTCTTAC TCCCTTTCTC 29340
TGTCTGTCTG TCGGTCTCTC TCTCTCTCTC TCCCTGTCTG TATGTTTCTC TCTGTCTCTG 29400
TCTCTCTCTC TCTTTCTGTT TCTCTCTCTC CGTCTCTGTC TTTCTCTGAC TGTCTCTCTC 29460
TTTCCTTCTC TCTGTCTCTC TCTGCCTGTC TCTCTCACTC TGTCTTCTGT CTTATCTCTC 29520
TCTCTGCCTG CCTGTCTCTC TCACTCTCTC TCTCTGTGTG TCTCTCTCTC TCTTTCTGTT 29580
TCTCTCTGTC TCTCTGTCCG TCTCTGTCTT TCTCTGTCTG TCTCTTTGTC TGTCTGTCTT 29640
TGTCTTTCCT TCTCTCTGTC TCTGTCTCTC TCACTGTGTC TGTCTTCTGT CTTAGTCTCT 29700
CTCTCTCTCT CTCCCTGTCT GTCTGTCTCT CTCTCTCTCT CCCCCTGTCT GTTTCTCTCT 29760
CTCTCTCTCT CTCTCTCTCT CTCTGTCTTT GTCTTTCTTT CTGTCTCTGT CTCTCTCTCT 29820
CTCTCTGTGT GTCTGTCTTC TGTCTTACTG TCTTTCTCTG CCTGTCTGTC TGTCTGTCTC 29880
```

-202-

```
TCTCTGTCTG TCTCTCTCTC TCTCTCCCCC TGTCGGCTGT TTCTCTGTCT CTGTCTGTGT  29940
CTCTCTTTCT GTCTGTTTCT CTCTGTCTGT CTTTCTCTCT CTGTCTCTTT CTCTCTGTCT  30000
CTCTGTCTGT CTCTGTCTCT CTCTCTGTCT CTCTCTCTCT GTGGGGGTGT GTGTGTGTGT  30060
GTGTATGTGT GTGTGTGTGT GTGTGTGTGT CTGCCTTCTG TCTTACTCTC TTTCTCTGCC  30120
TGTCTGTCTG CCTGTCTGTT TGTCTGTCTC TCTCTGCCTG TCTCTCTCCC TTCCTGTCTG  30180
TTTCTCTTCTC TTTCTGTTTC TCTCTGTCTC TGTCCATCTC TGTCTTTCTC CGTCTGTCTC  30240
TTTATCTGTC TCTCTCCGTC TGTCTCTTTA TCTGTCTCTC TCTCTCTTTC TGTCTTTCTC  30300
TCTCTGTGTA TCGTTGTCTC TCTCTGTCTG TCTCTGTCTC TGTCTCTCTG TCTCTCTCTC  30360
TCTCTCTCTC TCTCTGTCTG TCTGTCCGTC TGTCTGTCTC GGTCTCTGCG TCTCGCTATC  30420
TCCCGCCCTC TCTTTTTTTG CAAAAGAAGC TCAAGTACAT CTAATCTAAT CCCTTACCAA  30480
GGCCTGAATT CTTCACTTCT GACATCCCAG ATTTGATCTC CCTACAGAAT GCTGTACAGA  30540
ACTGGCGAGT TGATTTCTGG ACTTGGATAC CTCATAGAAA CTACATATGA ATAAAGATCC  30600
AATCCTAAAA TCTGGGGTGG CTTCTCCCTC GACTGTCTCG AAAAATCGTA CCTCTGTTCC  30660
CCTAGGATGC CGGAAGAGTT TTCTCAATGT GCATCTGCCC GTGTCCTAAG TGATCTGTGA  30720
CCGAGCCCTG TCCGTCCTGT CTCAAATATG TACGTGCAAA CACTTCTCTC CATTTCCACA  30780
ACTACCCACG GCCCCTTGTG GAACCACTGG CTCTTTGAAA AAAATCCCAG AAGTGGTTTT  30840
GGCTTTTTGG CTAGGAGGCC TAAGCCTGCT GAGAACTTTC CTGCCCAGGA TCCTCGGGAC  30900
CATGCTTGCT AGCGCTGGAT GAGTCTCTGG AAGGACGCAC GGGACTCCGC AAAGCTGACC  30960
TGTCCCACCG AGGTCAAATG GATACCTCTG CATTGGCCCG AGGCCTCCGA AGTACATCAC  31020
CGTCACCAAC CGTCACCGTC AGCATCCTTG TGAGCCTGCC CAAGGCCCCG CCTCCGGGGA  31080
GACTCTTGGG AGCCCGGCCT TCGTCGGCTA AAGTCCAAAG GGATGGTGAC TTCCACCCAC  31140
AAGGTCCCAC TGAACGGCGA AGATGTGGAG CGTAGGTCAG AGAGGGACC AGGAGGGGAG  31200
ACGTCCCGAC AGGCGACGAG TTCCCAAGGC TCTGGCCACC CCACCCACGC CCCACGCCCC  31260
ACGTCCCGGG CACCCGCGGG ACACCGCCGC TTTATCCCCT CCTCTGTCCA CAGCCGGCCC  31320
CACCCCACCA CGCAACCCAC GCACACACGC TGGAGGTTCC AAAACCACAC GGTGTGACTA  31380
GAGCCTGACG GAGCGAGAGC CCATTTCACG AGGTGGGAGG GGTGGGGGTG GGGTGGGTTG  31440
GGGGTTGTGG GGTCTGTGGC GAGCCCGATT CTCCCTCTTG GGTGGCTACA GGCTAGAAAT  31500
GAATATCGCT TCTTGGGGGG AGGGGCTTCC TTAGGCCATC ACCGCTTGCG GGACTACCTC  31560
TCAAACCCTC CCTTGAGGCC ACAAAATAGA TTCCACCCCA CCCATCGACG TTTCCCCCGG  31620
GTGCTGGATG TATCCTGTCA AGAGACCTGA GCCTGACACC GTCGAATTAA ACACCTTGAC  31680
TGGCTTTGTG TGTTTGTTTG TTTCTGAGAT GGAGTCTTGC TCTGTCCCCC AGGCTGGAGT  31740
GCAGTGGCGT GATCTCAGCT CACTGGAACC TCTGCCTCCT GGGTTCAAGT GATTCTCCTG  31800
TCTCAGCGCC ACCATGGCCG GCTCATTTTT .TTTTTTTTT TTTTTGGTAG ACACGGGGTT  31860
TCACCCTCTT TCATTGGTTT TCACTGGAGA TTCTAGATTC GAGCCACACC TCATTCCGTG  31920
CCACAGAGAG ACTTCTTTTT TTTTTTTTTT TTTTAAGCG CAACGCAACA TGTCTGCCTT  31980
ATTTGAGTGG CTTCCTATAT CATTATAATT GTGTTATAGA TGAAGAAACG GTATTAAACA  32040
CTGTGCTAAT GATAGTGAAA GTGAAGACAA AAGAAAGGCT ATCTATTTTG TGGTTAGAAT  32100
AAAGTTGCTC AGTATTTAGA AGCTACCTAA ATACGTCAGC ATTTACACTC TTCCTAGTAA  32160
AAGCTGGCCG ATCTGAATAA TCCTCCTTTA AACAAACACA ATTTTTGATA GGGTTAAGAT  32220
TTTTTAAGA ATGCGACTCC TGCAAAATAG CTGAACAGAC GATACACATT TAAAAAAATA  32280
ACAACACAAG GATCAACCAG ACTTGGGAAA AAATCGAAAA CCACACAAGT CTTATGAAGA  32340
ACTGAGTTCT TAAAATAGGA CGGAGAACGT AGCTATCGGA AGAGAAGGCA GTATTGGCAA  32400
GTTGATTGTT ACGTTGGTCA GCAGTAGCTG GCACTATCTT TTTGGCCATC TTTCGGGCAA  32460
TGTAACTACT ACAGCAAAAT GAGATATGAT CCATTAAACA ACATATTCGC AAATCAAAAA  32520
GTGTTTCAGT AATATAATGC TTCAGATTTA GAAGCAAATC AAATGATAGA ACTCCACTGC  32580
TGTAATAAGT CACCCCAAAG ATCACCGTAT CTGACAAAAT AACTACCACA GGGTTATGAC  32640
TTCAGAATCA TACTTTCTTC TTGATATTTA CTTATGTATT TATTTTTTTT AATTTATTTC  32700
TCTTGAGACG CGTCTCGCTC TGTCGCCCAG GCTGGAGTGC GATGGTGTGA TCTCGGCTCA  32760
CTGCAACCGC CACCTCCCTG GGTTCAAGCG ATTCTCCTGC CTCAGCCTCC CGAGTAGCTG  32820
GGACTACAGG TGCCCGCCAC CACGCCCAGC TAATCTTTAT ACTTTTAATA GAGACGGGGT  32880
TTCACCGTGT CGGCCCGGAT GGTCTCGATC TCTTGACCTC GTGACCCGCC CGCCTCGGCC  32940
TCCCAAAGTG CTGGGATGAC AGGCGTGAGC CACTGAGCCC GGCCTTCTCT TGACGTTTAA  33000
ACTATGAAGT CAGTCCAGAG AAACGCAATA AATGTCAACG GTGAGGATGG TGTTGAGGCA  33060
GAAGTAGGAC CACACTTTTT CCTATCTTAT TCAGTTGATA ACAATATGAC CTAGGTAGTA  33120
ATTTCCTATG TGCCTACTTA TACACGAGTA CAAAAGAGTA AAACAGAGAG ACTGCTAAAT  33180
TAAAGGGTAC GTGAAGTTCT TCATAGTAAC TCCGTAAACT GGAACACTGT CAAAAAGCAG  33240
CAGCTAGTGA ATTGTTTCCA TGTATTTTTC TATTATCCAA TAAGTGAACT ATGCTATTCC  33300
TTTCCAGTCT CCCAAGCACT TCTTGTCCCC ATCACCACTT CGGTGCTCGA AGAAAAAGTA  33360
AGCAAATCAA GGAACACAAG CTAAAGAAAC ACACACACAA ACCAAAGACA ACTACAGCGT  33420
CTGCAAAAGT TTGCTAGAAG ACTGAAACTG TTGAGTATAA GGATCTGGTA TTCTACGATC  33480
ATGAGTTCAC TTCAGAGTTT GTTCAAGACA TACGTTTCGT AAGGAAACAT CTTAGTTAGA  33540
AGTTATTCAG CAGTAGGTAC CATCCCTAAG TATTTTTCAC CAAATCCGTG ACAATAAAGA  33600
GCTATCTAAC CAGAAAAATT AGCGAGTACG GGCACCATCC ATAGGGCTTT GTCTTTACGC  33660
TTCATTAGCA CTTACCATGC CTTACAATGT CTAGGATTGA CCCTGATAGC ATTTCGAAAA  33720
CAAGCTAATG CTTTGTCCAG TTCTTCAGTG AAGACAACTC ACGCCCTAAT GCGCTATAGG  33780
CATAAGCATC ATTTGGATCC ACTTCGAGAG TTCTCTGGAA GAATTGAATC GCAATATCGT  33840
GTTCCCGTTT GCAGACCGAA ACAGTTTCCC TGCAGCACAC CAGGCCTCTG GCTGGCGAAT  33900
```

-203-

```
TTTTATCCAT GTCTGTGAAG TCTTTGGACA GAACTGAAAG AGCAACCTCT TTCGGAGGAT 33960
GCCAAAGTGT TGTAGAGTAG ATCTCCATGC CTTCGACTCT GTAATTCTCA ATCCTCCTAA 34020
CCTCTGAGAA TTGTCTTTCA GCTTGCGTGG ACTCTGAAAG TTTACAATAG GCCNTTTCCG 34080
ATTTGGCACA GTACCCAACC GGTATTGCAG TGGTGAGAAG CTAGATGGCT CAAGATGCTG 34140
ATAGCTTCTT TGCCGTGGTA AGAACACAAA GCTAAATAAC CTTTCCCCCT TTCACGAAGA 34200
AGGCTCATCA AGCCTTCCGC TGCTGCTTTT TGTAGATTAA AAGCCTGAAT CTGAGGCGCG 34260
ATTGCGGCTA TTTTCCCTTC TGAAATGACG GAAGAGTCCA ATTTTGTCAC TTCCAGGCTA 34320
TCACTTATGT TCGGTGGAGT TATTGCTCCT TTATTAGTTT TACTTTTGGT TCTTCTGTTT 34380
GGGATTTTAG GTGGAAACTT CATTTTTAAT TTTCTCCTAA TTCTCCTCGG TTGTGGAGCT 34440
GTCACTAGTC AAGAGTCGTG AATTTCTTCG AGGNCGGTGC ATTTGGGGGA GATGCCATAG 34500
TGGGGCTCAA TACCTGAGGT GTTGCCCTTG TCGGCGGACC AGAACTTTGT GTTTTTGCAA 34560
GGACTGGAGT TACCTTTCGG CTCTTTCCCC TCTGCGAGAA GACAGACGGT GTTCCGGTTT 34620
GGCCGATTCT GGCAACAGGC TTTTCTGAAG GGGCTCCGGT GGATGGCACG TCAGTGACAG 34680
ACGGTGTCTC ATACCAGTGC AGTTTTGTCA ATAGGGTCCG TCTCCGGGAC TTGGGGTTTC 34740
TAATGGCAAA ATGCCAACAC TTGGGGTTAA TGGACTAACA GCTGCTGGTC CTCCTAATAA 34800
ACTTCGACCA GTTTTTGGTT TATGTTGAAC CTGTTTAGAT CATATGGAAG TTCCTGTTCC 34860
CAGTGGGACA GTATCAGGTG AAAGGACAGC TGAATCGATA GAAGACACTG GGGAGTCTGT 34920
ATTCAAGGAG TACTTTGAAT TGGAAGATTC TAAATTCCAT CCGTTTCATT CGACGGTGTC 34980
CTGGGGTGTT TCCGTAAGAA CGGTCTCGGG CTGTCTGTGA CATAAACTAG GACGAGGTCC 35040
AAGTGTTGTG GCGCAACACT TGGACAGGCA GTTGCTAAAG CTCTCTAGAG AGGTGAATCA 35100
AAATGTTTGG TCAGGATCTG GCTTTTCCCC CCTATTTCAC ATCATGATTC AAAGGGACAC 35160
CAGAGGAAAG GATTTCAACG AAGGCTCTTT TGGTCACATT CTGATCCTTT GGTAAGCCGA 35220
TCTGTCTTGC AATATACATG TCCCGACGAT GGAAGGGGAA AGCGAGCTGA ATCACCAAAC 35280
TCAGGAACGA TAATATCATC GTGGCTTTTC TGCTTATGAA ACACTCCACC CGATAAGATT 35340
TGATCCCCTT CTGCAAGCTT GCTGAGATCA ACACAACATT TCGCAAGCAG GCATTTGCAT 35400
TGCGGGGTAG TACAACTGTG TCCTTTCAAG AGTCTATATG TTTTATAGGC CTTTCCTGAG 35460
CGGTAAGAAC AGGTCGCCAG TAAGAACAAG GCTTCTTCTG AGTGTACTTC TGCATAAAGG 35520
CGTTCTGCGG GGGAAACCGC ATCTCGGTAG GCATAGTGGT TTAGTGCTTG CCATATAGCA 35580
GCCTGGACGG GTCCCTGCAG CACCGCCATC CTCGAGGCTC AGGCCCACTT TCTGCAGTGC 35640
CACAGGCACC CCCCCCCCCC CATAGCGGCT CCGGCCCGGC CAGCCCCGGC TCATTTAAAG 35700
GCACCAGCCG CCGTTACCGG GGGATGGGGG AGTCCGAGAC AGAATGACTT CTTTATCCTG 35760
CTGACTCTGG AAAGCCCGGC GCCTTGTGAT CCATTGCAAA CCGAGAGTCA CCTCGTGTTT 35820
AGAACACGGA TCCACTCCCA AGTTCAGTGG GGGGATGTGA GGGGTGTGGC AGGTAGGACG 35880
AAGGACTCTC TTCCTTCTGA TTCGGTCTGC ACAGTGGGGC CTAGGGCTGG AGCTCTCTCC 35940
GTGCGGACCG CTGACTCCCT CTACCTTGGG TTCCCTCGGC CCCACCCTGG AACGCGGGGC 36000
CTTGGCAGAT TCTGGCCCTT TCTGGCCCTT CAGTCGCTGT CAGAAACCCC ATCTCATGCT 36060
CGGATGCCCC GAGTGACTGT GGCTCGCACC TCTCCGGAAA CATTGGAAAT CTCTCCTCTA 36120
CGCGCGGCCA CCTGAAACCA CAGGAGCTCG GGACACACGT GCTTTCGGGA GAGAATGCTG 36180
AGAGTCTCTC GCCGACTCTC TCTTGACTTG AGTTCTTCGT GGGTGCGTGG TTAAGACGTA 36240
GTGAGACCAG ATGTATTAAC TCAGGCCGGG TGCTGGTGGC TCACGCCTGT AACCCCAACA 36300
CTTTGGGAGG CCGAGGCCGT AGGATCCCTC GAGGAATCGC CTAACCCTGG GGAGGTTGAG 36360
GTTGCAGTGA GTGAGCCATA GTTGTGTCAC TGTGCTCCAG TCTGGGCGAA AGACAGAATG 36420
AGGCCCTGCC ACAGGCAGGC AGGCAGGCAG GCAGGCAGAA AGACAACAGC TGTATTATGT 36480
TCTTCTCAGG GTAGGAAGCA AAAATAACAG AATACAGCAC TTAATTAATT TTTTTTTTTT 36540
CCTTCGGACG GAGTTTCACT CTTGGTGCCC ACGCTGGAGT GCAGTGGCAC CATCTCGGCT 36600
CACCGCAACC TCCACCTCCC GCGTTCAAGC GATTCTCCTG CCTCAGCCTC CTGAGTAGCT 36660
GGGATTACAG GGAGGAGCCA CCACACCCAG CTGATTTTGT ATTGTTAGTA GAGACGGCAT 36720
TTCTCCATGT GGGTCAGGCT GGTCTCGAAC TGGCGACCCC AGTGGATCTG CCCGCCCCGG 36780
CCTCCCAAAG TGCTGGGGTG ACAGGCGTGA GCCATCGTGA CTGGCCGGCT ACGTTTATTT 36840
ATTTATTTTT TTAATTATTT TACTTTTTTT TAGTTTTCCA TTTTAATCTA TTTATTTATT 36900
TACATTTATT TATTTATTTA TTTATTTACT TATTTATTTA TTTTCGAGAC AGACTCTCGC 36960
TCTGCTGCCC AGGCTGGAGT GCAGCGGCGT GATCTCGGCT CACTGCAACG TCCGCCTCCC 37020
GGGTTCACGC CATTCTCCTG CCTCAGCCTC CCAAGTAGCT GGGACTACAG GCGCCCGCCA 37080
CCGTGCCCGG CTAACTTTTT GTATTTTTAG TAGAGATGGG GTTTCACTGT GGTAGCCAGG 37140
ATGGTCTCGA TCTCCTGACC CCGTGATCCG TCCACCTCGG CCTCCCAAAG TGCTGGGATG 37200
ACAGGCGTGA GCCACCGGCC CCGGCCTATT TATCTATTTA TTAACTTTGA GTCCAGGTTA 37260
TGAAACCAGT TAGTTTTTGT AATTTTTTTT TTTTTTTTTT TTTTTGAGA CGAGGTTTCA 37320
CCGTGTTGCC AAGGCTTGGA CCGAGGGATC CACCGGCCCT CGGCCTCCCA AAAGTGCGGG 37380
GATGACAGGC GCGAGCCTAC CGCGCCCGGA CCCCCCCTTT CCCCTTCCCC CGCTTGTCTT 37440
CCCGACAGAC AGTTTCACGG CAGAGCGTTT GGCTGGCGTG CTTAAACTCA TTCTAAATAG 37500
AAATTTGGGA CGTCAGCTTC TGGCCTCACG GACTCTGAGC CGAGGAGTCC CCTGGTCTGT 37560
CTATCACAGG ACCGTACACG TAAGGAGGAG AAAAATCGTA ACGTTCAAAG TCAGTCATTT 37620
TGTGATACAG AAATACACGG ATTCACCCAA AACACAGAAA CCAGTCTTTT AGAAATGGCC 37680
TTAGCCCTGG TGTCCGTCCC AGTGATTCTT TTCGGTTTGG ACCTTGACTG AGAGGATTCC 37740
CAGTCGGTCT CTCGGTCTCT GACGGAAGTT CCAGATGATC CGATCGGTGG GGGACTTAGG 37800
CTGCGTCCCC CCAGGAGCCC TGGTCGATTA GTTGTGGGGA TCGCCTTGGA GGGGCGCGGTG 37860
ACCCACTGTG CTGTGGGAGC CTCCATCCTT CCCCCCACCC CCTCCCCAGG GGGATCCCAA 37920
```

-204-

```
TTCATTCCGG GCTGACACGC TCACTGGCAG GCGTCGGGCA TCACCTAGCG GTCACTGTTA 37980
CTCTGAAAAC GGAGGCCTCA CAGAGGAAGG GAGCACCAGG CCGCCTGCGC ACAGCCTGGG 38040
GCAACTGTGT CTTCTCCACC GCCCCCGCCC CCACCTCCAA GTTCCTCCCT CCCTTGTTGC 38100
CTAGGAAATC GCCACTTTGA CGACCGGGTC TGATTGACCT TTGATCAGGC AAAAACGAAC 38160
AAACAGATAA ATAAATAAAA TAACACAAAA GTAACTAACT AAATAAAATA AGTCAATACA 38220
ACCCATTACA ATACAATAAG ATACGATACA ATAGGATGCG ATAGGATACG ATAGGATACA 38280
ATACAATAGG ATACGATACA ATACAATACA ATACAATACA ATACAATACA ATACAATACA 38340
ATACAATACA ATACAATACG CCGGGCGCGG TGGCTCATGC CTGTCATCCC GTCACTTTGG 38400
GATGCCGAGG TGGACGCATC ACCTGAAGTC GGGAGTTGGA GACAAGCCCG ACCAACATGG 38460
AGAAATCCCG TCTCAATTGA AAATACAAAA CTAGCCGGGC GCGGTGGCAC ATGCCTATAA 38520
TCCCAGCTGC TAGGAAGGCT GAGGCAGGAG AATCGCTTGA ACCTGGGAAG CGGAGGTTGC 38580
AGTGAGCCGA GATTGCGCCA TCGCACTCCA GTCTGAGCAA CAAGAGCGAA ACTCCGTCTC 38640
AAAAATAAAT ACATAAATAA ATACATACAT ACATACATAC ATACATACAT ACATACATAC 38700
ATAAATTAAA ATAAATAAAT AAAATAAAAT AAATAAATGG GCCCTGCGCG GTGGCTCAAG 38760
CCTGTCATCC CCTCACTTTG GGAGGCCAAG GCCGGTGGAT CAAGAGGCGG TCAGACCAAC 38820
AGGGCCAGTA TGGTGAAACC CCGTCTCTAC TCACAATACA CAACATTAGC CGGGCGCTGT 38880
GCTGTGCTGT ACTGTCTGTA ATCCCAGCTA CTCGGGAGGC CGAGCTGAGG CAGGAGAATC 38940
GCTTGAACCT GGGAGGCGGA GGTTGCAGTG AGCCGAGATC GCGCCACTGC AACCCAGCCT 39000
GGGCGACAGA GCGAGACTCC GTCTCCAAAA AATGAAAATG AAAATGAAAC GCAACAAAAT 39060
AATTAAAAAG TGAGTTTCTG GGGAAAAAGA AGAAAAGAAA AAAGAAAAAA ACAACAAAAC 39120
AGAACAACCC CACCGTGACA TACACGTACG CTTCTCGCCT TTCGAGGCCT CAAACACGTT 39180
AGGAATTATG CGTGATTTCT TTTTTAACT TCATTTATG TTATTATCAT GATTGATGTT 39240
TCGAGACGGA GTCTCGGAGG CCCGCCCTCC CTGGTTGCCC AGACAACCCC GGGAGACAGA 39300
CCCTGGCTGG GCCCGATTGT TCTTCTCCTT GGTCAGGGGT TTCCTTGTCT TTCTTCGTGT 39360
CTTTAACCCG CGTGGACTCT TCCGCCTCGG GTTTGACAGA TGGCAGCTCC ACTTTAGGCC 39420
TTGTTGTTGT TGGGGACTTT CCTGATTCTC CCCAGATGTA GTGAAAGCAG GTAGATTGCC 39480
TTGCCTGGCC TTGCCTGGCC TTGCCTTTTC TTTCTTTCTT TCTTTCTTTA TTACTTTCTC 39540
TTTTTCTTCT TCTTCTTCTT CTTTTTTTTG AGACAGAGTT TCACTCTTGT TGCCCAGGCT 39600
AGAGGGCAAT GGCGCGATCT CGGCTCACCG CACCCTCCGC CTCCCAGGTT CAAGCGATTC 39660
TCCTGCCTCA GCCTCCTGAT TAGCTGGGAT TACAGGCATG GGCCACCGTG CTGGCTGATG 39720
TTTGTACTTT TAGTAGAGAC GGTGTTTTTC CATGTTGGTC AGGCTGGTCT CCCACTCCCA 39780
ACCTCAGGTG GTCCGCCTGC CTTAGCCTCC CAAAGTGCTG GGATGACAGG CGTGCAACCG 39840
CGCCCAGCCT CTCTCTCTCT CTCTCTCTCT CTCGCTCGCT TGCTTGCTTG CTTTCGTGCT 39900
TTCTTGCTTT CCCGTTTTCT TGCTTTCTTT CTTTCTTTCG TTTCTTTCAT GCTTGCTTTC 39960
TTGCTTGCTT GCTTGCTTTC GTGCTTTCTT GCTTTCCTGT TTTCTTTCTT TCTTTCTTTC 40020
TTTCTTTCTT TTGTTTCTTT CTTGCTTGTT GCTTGCTTTC CTTGCTGTTT TCGTGCTTT 40080
CTTGCTTTCC TGTTTTCTTT CTTTCTTTCT TTCTTTTCTT TCTTTCTTGC TTGCTTTCCT 40140
GCTTGCTTGC TTTCGTGCTT TCTTGTTTTC TCGATTTCTT TCTTTCTTTT GTTTCTTTCC 40200
TGCTTGCTTT CTTGCTTGCT TGCTTTCGTG CTTCTTGCTT TCCTGTTTTC TTTCTTTCTT 40260
TCTTTCTTTT GTTTCTTTCT TGCTTGCTTT CTTGCTTGCT TGCTTTCGTG CTGTCTTGTT 40320
TCTCGATTTC TTTCTTTCTT TTGTTTCTTT CCTGCTTGCT TTCTTGCTTG ATTGCTTTCG 40380
TGCTTTCTTG CTTTCTTGTT TTCTTTCTTT CTTTTGTTTC TTTCTTTCTT GCTTCCTTGT 40440
TTTCTTGCTT TCTTGCTTGC TTGCTTTCGT GCTTTCTTGT TTTCTTGCTT TCTTTCTTTT 40500
GTTTCTTTCT TGCTTGCTTT CTTGCTTCCT TGTTTCTTG CTTTCTTGCT TGCTTGCTTT 40560
CGTGCTTTCT TTCTTGCTTT CTTTTCTTTC TTTCTTTTCT TTTTCTTTCT TTCTTGCTTT 40620
CTTTTCTTTC ATCATCATCT TTCTTTCTTT CCTTTCTTTC TTTCTTTCTT TCTATCTTTC 40680
TTTCTTTCTT TCTTTCTTTC TTTCTTTCTT TCTTTCTGTT TCGTCCTTTT GAGACAGAGT 40740
TTCACTCTTG TTTCCACGGC TAGAGTGCAA TGGCGCGATC TTGGCTCACC GCACCTTCCG 40800
CCTCCCGGGT TCGAGCGCTT CTCCTGCCTC CAGCCTCCCG ATTAGCGGGG ATTGACAGGG 40860
AGGCACCCCC ACGCCTGGCT TGGCTGATGT TTGTGTTTTT AGTAGGCACG CCGTGTCTCT 40920
CCATGTTGCT CAGGCTGGTC TCCAACTCCC GACCTCCTGT GATGCGCCCA CCTCGGCCTC 40980
TCGAAGTGCT GGGATGACGG GCGTGACGAC CGTGCCCGGC CTGTTGACTC ATTTCGCTTT 41040
TTTATTTCTT TCGTTTCCAC GCGTTTACTT ATATGTATTA ATGTAAACGT TTCTGTACGC 41100
TTATATGCAA ACAACGACAA CGTGTATCTC TGCATTGAAT ACTCTTGCGT ATGGTAAATA 41160
CGTATCGGTT GTATGGAAAT AGACTTCTGT ATGATAGATG TAGGTGTCTG TGTTATACAA 41220
ATAAATACAC ATCGCTCTAT AAAGAAGGGA TCGTCGATAA AGACGTTTAT TTTACGTATG 41280
AAAAGCGTCG TATTTATGTG TGTAAATGAA CCGAGCGTAC GTAGTTATCT CTGTTTTCTT 41340
TCTTCCTCTC CTTCGTGTTT TTCTTCCTTC CTTTCTTCCT TTCTCTCCTT CTTTAGGTTT 41400
TTCTTCCTCT CTTCCTTTCC TTCTTTCTCT CTTTCTGTCC TTTTTTCCTT CGTGCTTTAT 41460
TTCTCTTTCG TTCCCTGTGT TTCCTTCTTT TTTCTTTCCT CTCTGTTTCT TTTTCCCTTC 41520
TTTCCTTCGT TTCTTTCCTC ATTCTTTCTC TCTTTTTCGT TGTTTCTTTC CTTCCCGTCT 41580
GTCTTTTAAA AAATTGGAGT GTTTCAGAAG TTTACTTTGT GTATCTACGT TTTCTAAATT 41640
GTCTCTCTTT TCTCCATTTT CTTCCTCCCT CCCTCCCTCC CTCCCTGCTC CCTTCCCTCC 41700
CTCCTTCCCT TTCGCCATCT GTCTCTTTTC CCCACTCCCC TCCCCCGTC TGTCTCTGCG 41760
TGGATTCCGG AAGAGCCTAC CGATTCTGCC TCTCCGTGTG TCTGCAGCGA CCCCGCGACC 41820
GAGTCCTTGT GTGTTCTTTC TCCCTCCCTC CCTCCCTCCC TCCCTCCCTC CCTCCCTGCT 41880
TCCGAGAGGC ATCTCCAGAG ACCGCGCCGT GGGTTGTCTT CTGACTCTGT CGCGGTCGAG 41940
```

```
GCAGAGACGC GTTTTGGGCA CCGTTTGTGT GGGGTTGGGG CAGAGGGGCT GCGTTTTCGG    42000
CCTCGGGAAG AGCTTCTCGA CTCACGGTTT CGCTTTCGCG GTCCACGGGC CGCCCTGCCA    42060
GCCGGATCTG TCTCGCTGAC GTCCGCGGCG GTTGTCGGGC TCCATCTGGC GGCCGCTTTG    42120
AGATCGTGCT CTCGGCTTCC GGAGCTGCGG TGGCAGCTGC CGAGGGAGGG GACCGTCCCC    42180
GCTGTGAGCT AGGCAGAGCT CCGGAAAGCC CGCGGTCGTC AGCCCGGCTG GCCCGGTGGC    42240
GCCAGAGCTG TGGCCGGTCG CTTGTGAGTC ACAGCTCTGG CGTGCAGGTT TATGTGGGGG    42300
AGAGGCTGTC GCTGCGCTTC TGGGCCCGCG GCGGGCGTGG GGCTGCCCGG GCCGGTCGAC    42360
CAGCGCGCCG TAGCTCCCGA GGCCCGAGCC GCGACCCGGC GGACCCGCCG CGCGTGGCGG    42420
AGGCTGGGGA CGCCCTTCCC GGCCCGGTCG CGGTCCGCTC ATCCTGGCCG TCTGAGGCGG    42480
CGGCCGAATT CGTTTCCGAG ATCCCCGTGG GGAGCCGGGG ACCGTCCCGC CCCCGTCCCC    42540
CGGGTGCCGG GGAGCGGTCC CCGGGCCGGG CCGCGGTCCC TCTGCCGCGA TCCTTTCTGG    42600
CGAGTCCCCG TGGCCAGTCG GAGAGCGCTC CCTGAGCCGG TGCGGCCCGA GAGGTCGCGC    42660
TGGCCGGCCT TCGGTCCCTC GTGTGTCCCG GTCGTAGGAG GGGCCGGCCG AAAATGCTTC    42720
CGGCTCCCGC TCTGGAGACA CGGGCCGGCC CCTGCGTGTG GCCAGGGCGG CCGGGAGGGC    42780
TCCCCGGCCC GGCGCTGTCC CCGCGTGTGT CCTTGGGTTG ACCAGAGGGA CCCCGGGCGC    42840
TCCGTGTGTG GCTGCGATGG TGGCGTTTTT GGGGACAGGT GTCCGTGTCC GTGTCGCGCG    42900
TCGCCTGGGC CGGCGGCGTG GTCGGTGACG CGACCTCCCG GCCCCGGGGG AGGTATATCT    42960
TTCGCTCCGA GTCGGCAATT TTGGGCCGCC GGGTTATAT                           42999
```

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 175 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
   (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:

    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
CTCCCGCGCG GCCCCGTGT TCGCCGTTCC CGTGGCGCGG ACAATGCGGT TGTGCGTCCA    60
CGTGTGCGTG TCCGTGCAGT GCCGTTGTGG AGTGCCTCGC TCTCCTCCTC CTCCCCGGCA    120
GCGTTCCCAC GGTTGGGGAC CACCGGTGAC CTCGCCCTCT TCGGGCCTGG ATCCG        175
```

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 755 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
   (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
GGTCTGGTGG GAATTGTTGA CCTCGCTCTC GGGTGCGGCC TTTGGGGAAC GGCGGGGTCG    60
GTCGTGCCCG CGCCGGACG TGTGTCGGGG CCCACTTCCC GCTCGAGGGT GGCGGTGGCG    120
GCGGCGTTGG TAGTCTCCCG TGTTGCGTCT TCCCGGGCTC TTGGGGGGGG TGCCGTCGTT    180
TTCGGGGCCG GCGTTGCTTG GCTTACGCAG GCTTGGTTTG GGACTGCCTC AGGAGTCGTG    240
GGCGGTGTGA TTCCCGCCGG TTTTGCCTCG CGTCTGCCTG CTTTGCCTCG GGTTTGCTTG    300
GTTCGTGTCT CGGGAGCGGT GGTTTTTTTT TTTTCGGGT CCCGGGGAGA GGGGTTTTTC    360
CGGGGGACGT TCCCGTCGCC CCCTGCCGCC GGTGGGTTTT CGTTTCGGGC TGTGTTCGTT    420
TCCCCTTCCC CGTTTCGCTC TCGGTTCTCC CCGGTCGGTC GGCCCTCTCC CCGGTCGGTC    480
GCCCGGCCGT GCTGCCGGAC CCCCCCTTCT GGGGGGGATG CCCGGGCACG CACGCGTCCG    540
GGCGGCCACT GTGGTCCGGG AGCTGCTCGG CAGGCGGGTG AGCCAGTTGG AGGGGCGTCA    600
TGCCCCCGCG GGCTCCCGTG GCCGACGCGG CGTGTTCTTT GGGGGGGGCCT GTGCGTGCGG    660
```

-206-

```
GAAGGCTGCG CACGTTGTCG GTCCTTGCGA GGGAAAGAGG CTTTTTTTTT TTAGGGGGTC        720
GTCCTTCGTC GTCCCGTCGG CGGTGGATCC GGCCT                                   755
```

    (2) INFORMATION FOR SEQ ID NO:20:

        (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 463 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
     (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
GGCCGAGGTG CGTCTGCGGG TTGGGGCTCG TCCGGCCCCG TCGTCCTCCG GGAAGGCGTT         60
TAGCGGGTAC CGTCGCCGCG CCGAGGTGGG CGCACGTCGG TGAGATAACC CCGAGCGTGT        120
TTCTGGTTGT TGGCGGCGGG GGCTCCGGTC GATGTCTTCC CCTCCCCCTC TCCCCGAGGC        180
CAGGTCAGCC TCCGCCTGTG GGCTTCGTCG GCCGTCTCCC CCCCCCTCAC GTCCCTCGCG        240
AGCGAGCCCG TCCGTTCGAC CTTCCTTCCG CCTTCCCCCC ATCTTTCCGC GCTCCGTTGG        300
CCCCGGGGTT TTCACGGCGC CCCCCACGCT CCTCCGCCTC TCCGCCCGTG GTTTGGACGC        360
CTGGTTCCGG TCTCCCCGCC AAACCCCGGT TGGGTTGGTC TCCGGCCCCG GCTTGCTCTT        420
CGGGTCTCCC AACCCCCGGC CGGAAGGGTT CGGGGGTTCC GGG                          463
```

    (2) INFORMATION FOR SEQ ID NO:21:

        (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 378 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
     (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
GGATTCTTCA GGATTGAAAC CCAAACCGGT TCAGTTTCCT TTCCGGCTCC GGCCGGGGGG         60
GGCGGCCCCG GGCGGTTTGG TGAGTTAGAT AACCTCGGGC CGATCGCACG CCCCCCGTGG        120
CGGCGACGAC CCATTCGAAC GTCTGCCCTA TCAACTTTCG ATGGTAGTCG ATGTGCCTAC        180
CATGGTGACC ACGGGTGACG GGGAATCAGG GTTCGATTCC GGAGAGGGAG CCTGAGAAAC        240
GGCTACCACA TCCAAGGAAG GCAGCAGGCG CGCAAATTAC CCACTCCCGA CCCGGGGAGG        300
TAGTGACGAA AAATAACAAT ACAGGACTCT TTCGAGGCCC TGTAATTGGA ATGAGTCCAC        360
TTTAAATCCT TTAAGCAG                                                      378
```

    (2) INFORMATION FOR SEQ ID NO:22:

        (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 378 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: Genomic DNA
    (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
     (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
GATCCATTGG AGGGCAAGTC TGGTGCCAGC AGCCGCGGTA ATTCCAGCTC CAATAGCGTA    60
TATTAAAGTT GCTGCAGTTA AAAAGCTCGT AGTTGGATCT TGGGAGCGGG CGGGCGGTCC   120
GCCGCGAGGC GAGTCACCGC CCGTCCCCGC CCCTTGCCTC TCGGCGCCCC CTCGATGCTC   180
TTAGCTGAGT TGTCCCGCGG GGCCCGAAGC GTTTACTTTG AAAAAATTAG AGTTGTTTCA   240
AAGCAGGCCC GAGCCGCCTG GATACCGCCA GCTAGGAAAT AATGGAATAG GACCGCGGTT   300
CCTATTTTGT TTGGTTTTCG GAACTGAGCC CATGATTAAG GGAAACGGCC GGGGGCATTC   360
CCTTATTGCG CCCCCCTA                                                 378
```

    (2) INFORMATION FOR SEQ ID NO:23:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 719 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: Genomic DNA
      (iii) HYPOTHETICAL: NO
       (iv) ANTI-SENSE: NO
        (v) FRAGMENT TYPE:
       (vi) ORIGINAL SOURCE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```
GGATCTTTCC CGCTCCCCGT TCCTCCCGGC CCCTCCACCC GCGCGTCTCC CCCCTTCTTT    60
TCCCCTCTCC GGAGGGGGGG GAGGTGGGGG CGCGTGGGCG GGGTCGGGGG TGGGGTCGGC   120
GGGGGACCGC CCCCGGCCGG CAAAAGGCCG CCGCCGGGCG CACTTCAACC GTAGCGGTGC   180
GCCGCGACCG GCTACGAGAC GGCTGGGAAG GCCCGACGGG GAATGTGGCT CGGGGGGGGC   240
GGCGCGTCTC AGGGCGCGCC GAACCACCTC ACCCCGAGTG TTACAGCCCT CCGGCCGCGC   300
TTTCGCGGAA TCCCGGGGCC GAGGGGAAGC CCGATACCCG TCGCCGCGCT TTTCCCCTCC   360
CCCCGTCCGC CTCCCGGGCG GGCGTGGGGG TGGGGCCGG GCCGCCCCTC CCACGCCCGT   420
GGTTTCTCTC TCTCCCGGTC TCGGCCGGTT TGGGGGGGGG AGCCCGGTTG GGGGCGGGGC   480
GGACTGTCCT CAGTGCGCCC CGGGCGTCGT CGCGCCGTCG GGCCCGGGGG GTTCTCTCGG   540
TCACGCCGCC CCCGACGAAG CCGAGCGCAC GGGGTCGGCG GCGATGTCGG CTACCCACCC   600
GACCCGTCTT GAAACACGGA CCAAGGAGTC TAACGCGTGC GCGAGTCAGG GGCTCGCACG   660
AAAGCCGCCG TGGCGCAATG AAGGTGAAGG GCCCCGTCCG GGGGCCCGAG GTGGGATCC    719
```

    (2) INFORMATION FOR SEQ ID NO:24:

        (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 685 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: Genomic DNA
      (iii) HYPOTHETICAL: NO
       (iv) ANTI-SENSE: NO
        (v) FRAGMENT TYPE:
       (vi) ORIGINAL SOURCE:

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
CGAGGCCTCT CCAGTCCGCC GAGGGCGCAC CACCGGCCCG TCTCGCCCGC CGCGTCGGGG    60
AGGTGGAGCA CGAGCGTACG CGTTAGGACC CGAAAGATGG TGAACTATGC CTGGGCAGGG   120
CGAAGCCAGA GGAAACTCTG GTGGAGGTCC GTAGCGGTCC TGACGTGCAA ATCGGTCGTC   180
CGACCTGGGT ATAGGGGCGA AAGACTAATC GAACCATCTA GTAGCTGGTT CCCTCCGAAG   240
TTTCCCTCAG GATAGCTGGC GCTCTCGCAA CCTTCGGAAG CAGTTTTATC CGGGTAAAGG   300
CGGAATGGAT TAGGAGGTCT TGGGGCCGGA AACGATCTCA AACTATTTCT CAAACTTTAA   360
ATGGGTAAGG AAGCCCGGCT CGCTGGCGTG GAGCCGGGCG TGGAATGCGA GTGCCTAGTG   420
GGCCACTTTT GGTAAGCAGA ACTGGCGCTG CGGGATGAAC CGAACGCCGG GTTAAGGCGC   480
CCGATGCCGA CGCTCATCAG ACCCCAGAAA AGGTGTTGGT TGATATAGAC AGCAGGACGG   540
TGGCCATGGA AGTCGGAATC CGCTAAGGAG TGTGTAACAA CTCACCTGCC GAATCAACTA   600
GCCCTGAAAA TGGATGGCGC TGGAGCGTCG GGCCCATACC CGGCCGTCGC CGGCAGTCGG   660
AACGGGACGG GACGGGAGCG GCCGC                                         685
```

-208-

(2) INFORMATION FOR SEQ ID NO:25:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 33 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG   33

(2) INFORMATION FOR SEQ ID NO:26:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 35 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG   35

(2) INFORMATION FOR SEQ ID NO:27:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 33 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC   33

(2) INFORMATION FOR SEQ ID NO:28:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 34 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
   (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
   (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC   34

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 80 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCCT AACCCTAACC CTAACCCTAA   60
CCCTAACCCT AACCCGGGAT   80

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 19 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG   19

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 25 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: Genomic DNA
  (iii) HYPOTHETICAL: NO
    (iv) ANTI-SENSE: NO
    (v) FRAGMENT TYPE:
    (vi) ORIGINAL SOURCE:

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT   25

(2) INFORMATION FOR SEQ ID NO:32:

    (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

```
        (ii)  MOLECULE TYPE: Genomic DNA
       (iii)  HYPOTHETICAL: NO
        (iv)  ANTI-SENSE: NO
         (v)  FRAGMENT TYPE:
        (vi)  ORIGINAL SOURCE:

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC                                                    26

    (2)  INFORMATION FOR SEQ ID NO:33:

         (i)  SEQUENCE CHARACTERISTICS:
         (A)  LENGTH: 26 base pairs
         (B)  TYPE: nucleic acid
         (C)  STRANDEDNESS: single
         (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: Genomic DNA
       (iii)  HYPOTHETICAL: NO
        (iv)  ANTI-SENSE: NO
         (v)  FRAGMENT TYPE:
        (vi)  ORIGINAL SOURCE:

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT                                                    26

    (2)  INFORMATION FOR SEQ ID NO:34:

         (i)  SEQUENCE CHARACTERISTICS:
         (A)  LENGTH: 21 base pairs
         (B)  TYPE: nucleic acid
         (C)  STRANDEDNESS: single
         (D)  TOPOLOGY: linear

        (ii)  MOLECULE TYPE: Genomic DNA
       (iii)  HYPOTHETICAL: NO
        (iv)  ANTI-SENSE: NO
         (v)  FRAGMENT TYPE:
        (vi)  ORIGINAL SOURCE:

        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A                                                         21
```